

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:42:19 ; Search time 41 Seconds

(without alignments)

877.685 Million cell updates/sec

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283415

Post-processing: Minimum Match 0% , Maximum Match 99.999%

Listing first 1045 summaries

Database : PIR_80;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1651.5	83.8	360	2	JC2443	chemokine (C-C) receptor
2	1224	62.1	352	2	A45113	chemokine (C-C) receptor
3	967.5	49.1	355	2	A45177	chemokine (C-C) receptor
4	960	48.7	359	2	I49341	MIP-1 alpha receptor
5	903.5	45.8	355	2	I49339	macrophage inflammatory protein-1 receptor
6	890.5	45.2	355	2	G02436	chemokine (C-C) receptor
7	833	42.3	360	2	JC4587	chemokine (C-C) receptor
8	831	42.2	360	2	JC1610	chemokine (C-C) receptor
9	794.5	40.3	383	2	S55594	G protein-coupled receptor
10	731	37.1	356	2	I49340	MIP-1 alpha receptor
11	723	36.7	357	2	JC5067	G protein-coupled receptor
12	704.5	35.8	354	2	I58186	probable G protein-coupled receptor
13	698	35.4	355	2	JC4304	orphan G protein-coupled receptor
14	644.5	32.7	344	2	JC5942	chemokine receptor
15	584	29.6	378	2	B55735	lymphocyte-specific receptor
16	575.5	29.2	378	2	A55735	G protein-coupled receptor
17	570	28.9	378	2	A45680	G protein-coupled receptor
18	554.5	28.1	369	2	JC5068	G protein-coupled receptor
19	541.5	27.5	360	2	A53611	interleukin-8 receptor
20	537	27.3	359	2	A48921	interleukin-8 receptor
21	531	27.0	352	2	G00048	fusion (LURSTR) - C receptor
22	530.5	26.9	353	2	S28787	neuropeptide Y receptor
23	529	26.9	355	2	JQ1231	interleukin-8 receptor
24	528	26.8	352	2	A45747	neuropeptide Y receptor
25	526	26.7	358	2	A53752	interleukin-8 receptor
26	526	26.6	367	2	A30349	interleukin-8 receptor
27	524.5	26.6	350	2	A39445	interleukin-8 receptor
28	523	26.5	356	2	S42096	G protein-coupled receptor
29	519	26.3	333	2	I65989	probable alatasta

30	484	24.6	359	2	JN0621	G protein-coupled angiotensin II receptor
31	480	24.4	359	2	A42656	G protein-coupled angiotensin II receptor
32	479.5	24.3	374	2	S42628	angiotensin II receptor
33	475	24.1	359	2	JC2134	angiotensin II receptor
34	473	24.0	359	2	JH0821	angiotensin II receptor
35	472	24.0	359	2	S15403	angiotensin II receptor
36	471	23.9	359	2	JQ1516	angiotensin II receptor
37	471	23.9	359	2	JC1104	angiotensin II receptor
38	469	23.8	359	2	S4425	angiotensin II receptor
39	468	23.8	359	2	JC1194	angiotensin II receptor
40	465	23.6	359	2	I39418	angiotensin II receptor
41	465	23.6	374	2	QQB623	HHRF3 protein - human
42	464	23.6	359	2	A49022	G protein-coupled angiotensin II receptor
43	461.5	23.4	372	2	S26667	G protein-coupled MDRP15 protein - human
44	460.5	23.4	327	2	S56162	G protein-coupled angiotensin II receptor
45	456	23.1	354	2	T09353	angiotensin II receptor
46	456	23.1	359	2	I39418	angiotensin II receptor
47	450	22.8	323	1	QQB623	HHRF3 protein - human
48	449.5	22.8	363	2	I48281	angiotensin II receptor
49	442.5	22.5	363	2	JC2543	angiotensin II receptor
50	438.5	22.3	363	2	A23659	angiotensin II receptor
51	433.5	22.0	362	2	JN0624	angiotensin II receptor
52	425	21.6	354	2	A23659	angiotensin II receptor
53	413	21.0	362	2	A30341	G protein-coupled kappa opioid receptor
54	410	20.8	362	2	A39714	interleukin-8 receptor
55	409	20.8	380	2	A48277	G protein-coupled kappa opioid receptor
56	408	20.7	380	2	S36143	beta opioid receptor
57	407	20.7	380	2	A55259	delta opioid receptor
58	406	20.6	380	2	JC2338	delta opioid receptor
59	405	20.1	380	2	JC2434	delta opioid receptor
60	395.5	20.1	388	2	JN0615	delta opioid receptor
61	392.5	19.9	384	2	A47249	delta opioid receptor
62	392	19.9	354	2	B55733	delta opioid receptor
63	386.5	19.6	384	2	JC4629	delta opioid receptor
64	381.5	19.4	364	2	JQ1488	delta opioid receptor
65	380.5	19.3	308	2	I50241	delta opioid receptor
66	373.5	19.0	367	2	JC2421	delta opioid receptor
67	373.5	19.0	367	2	I49022	delta opioid receptor
68	373.5	19.0	367	2	I56520	delta opioid receptor
69	373	18.9	363	2	I57955	delta opioid receptor
70	373	18.9	364	2	JN0763	delta opioid receptor
71	373	18.9	370	2	S43087	delta opioid receptor
72	372	18.9	370	2	T09508	delta opioid receptor
73	370.5	18.8	344	2	S34592	delta opioid receptor
74	369.5	18.8	372	2	S34592	delta opioid receptor
75	369	18.7	333	2	A57510	mu opioid receptor
76	368.5	18.7	398	2	I49519	mu opioid receptor
77	368	18.7	366	1	ODRPB2	bradykinin receptor
78	367.5	18.7	380	2	I38435	angiotensin receptor
79	365.5	18.6	398	2	I56504	mu opioid receptor
80	365	18.5	392	2	S65593	mu opioid receptor
81	363.5	18.5	398	2	I56511	mu opioid receptor
82	363	18.4	391	2	A41195	delta opioid receptor
83	363	18.4	391	2	C41795	delta opioid receptor
84	363	18.4	391	2	A39297	delta opioid receptor
85	362.5	18.4	372	2	I38332	delta opioid receptor
86	362.5	18.4	400	2	I56533	mu opiate receptor
87	362	18.4	352	2	S6004	mu opiate receptor
88	359.5	18.2	371	2	JC5796	N-formyl peptide C receptor
89	359.5	18.2	373	2	JE0087	probable chemoattractant receptor
90	358.5	17.6	423	2	JC6777	delta opioid receptor
91	357	18.1	363	2	B48227	delta opioid receptor
92	356	18.1	353	2	A53858	bradykinin receptor
93	355	18.0	364	2	A4952	N-formyl peptide C receptor
94	355	18.0	371	2	JC5796	probable chemoattractant receptor
95	355	18.0	373	2	JE0087	delta opioid receptor
96	346.5	17.6	423	2	B48227	delta opioid receptor
97	345.5	17.5	361	2	B45610	thrombin receptor
98	345	17.5	420	2	I51667	delta opioid receptor
99	345.5	17.4	369	2	JC2083	delta opioid receptor
100	341	17.3	369	2	D4175	delta opioid receptor
101	339	17.2	346	2	S29748	delta opioid receptor
102	339	17.2	357	2	JC7319	probable alatasta receptor

103	339	17.2	428	2	S30508	probable G protein	519	2	S17783
104	338	17.2	428	2	A440795	somatostatin recep	268	5	13.6
105	338	17.2	369	2	B41795	somatostatin recep	176	5	13.6
106	338	17.2	369	2	A45291	somatostatin recep	177	5	13.6
107	334	17.0	394	2	JC7249	galanin receptor -	265	5	13.5
108	332	16.9	370	2	JC5549	heptahelical P2Y5-	178	266	13.5
109	328	16.6	373	2	JC4737	G protein-coupled	179	265	13.5
110	327	16.6	328	2	JC8973	G protein-coupled	180	265	13.5
111	326	16.6	351	2	B42005	PMP-related recep	181	265	13.5
112	325	16.5	355	2	A55733	G protein-coupled	182	263	13.4
113	325	16.5	399	2	A48705	proteinase activat	183	262	13.3
114	324	16.5	353	2	JC2495	G protein-coupled	184	262	13.3
115	324	16.5	427	2	S17148	alpha-thrombin rec	185	262	13.3
116	324	16.4	373	2	JC4162	P2Y receptor - bov	186	261	13.3
117	322	16.4	342	2	S13638	platelet-activatin	187	260	13.2
118	321	16.3	334	2	JC4681	bradykinin B1 rece	188	260	13.2
119	320	16.3	350	2	A42009	N-formyl peptide r	189	260	13.2
120	317	16.1	362	2	S33733	G protein-coupled	190	260	13.2
121	315	16.0	359	2	JC5227	G protein-coupled	191	260	13.2
122	314	16.0	352	1	S2357	complement C5a ana	192	258	13.1
123	314	15.9	360	2	G02064	G protein-coupled	193	258	13.1
124	312	15.9	342	2	A40191	platelet-activatin	194	258	13.1
125	310	15.8	351	2	JC7086	leukotriene B4 rec	195	257	13.0
126	309	15.7	350	1	A37963	complement C5a ana	196	256	13.0
127	308	15.6	397	2	JC5949	galanin receptor 2	197	255	13.0
128	307	15.6	397	2	S6518	proteinase-activat	198	255	13.0
129	306	15.6	352	2	A46520	N-formyl peptide r	199	255	12.9
130	305	15.5	449	2	A41758	neuropeptide Y rec	200	254	12.9
131	304	15.5	422	2	JC7080	melanin-concentrat	201	254	12.9
132	304	15.4	351	2	A46525	complement C5a ana	202	254	12.9
133	303	15.4	352	2	JB0296	thyrotropin releas	203	254	12.9
134	302	15.3	432	2	A43448	thyrotropin receptor	204	254	12.9
135	301	15.3	375	2	JC5069	G protein-coupled	205	254	12.9
136	301	15.3	365	2	S68679	G protein-coupled	206	253	12.9
137	300	15.2	341	2	S63666	platelet activatin	207	253	12.8
138	300	15.2	430	2	A15895	complement C5a ana	208	253	12.8
139	298	15.2	390	2	JH0374	galanin receptor 2	209	252	12.8
140	296	15.0	341	2	S4252	platelet-activatin	210	252	12.8
141	295	15.0	423	2	B40470	G protein-coupled	211	252	12.8
142	294	14.9	349	2	I59336	G protein-coupled	212	250	12.7
143	294	14.9	375	2	A55509	cholecystokinin A	213	249	12.7
144	294	14.9	411	2	I56444	bombesin receptor	214	248	12.6
145	294	14.9	412	2	S23435	platelet-activatin	215	248	12.6
146	295	14.8	365	2	S68208	glucocorticoid-ind	216	247	12.6
147	289	14.7	398	2	JN0692	galanin receptor 1	217	247	12.5
148	289	14.7	444	2	T27866	G protein-coupled	218	244	12.4
149	286	14.5	395	2	S40685	thyrotropin-releas	219	244	12.4
150	285	14.5	387	2	I69202	thyrolyberin recep	220	244	12.3
151	284	14.5	387	2	I55450	G protein-coupled	221	243	12.3
152	283	14.4	390	2	B41007	bombesin receptor	222	243	12.3
153	283	14.4	428	2	JN0692	thyrotropin-releas	223	243	12.3
154	283	14.4	425	2	A37912	hypothetical prote	224	242	12.2
155	282	14.3	584	2	JC7809	probable G protein	225	242	12.2
156	281	14.3	393	2	A39251	G protein-coupled	226	242	12.2
157	281	14.3	362	2	B57641	G protein-coupled	227	242	12.2
158	277	14.1	404	2	JC5784	PMP-related recep	228	242	12.1
159	280	14.2	444	2	S00516	adrenomedullin rec	229	242	12.1
160	280	14.2	425	2	I53033	cholecystokinin ty	230	242	12.0
161	276	14.0	354	2	G02670	sulfakinin recepto	231	242	12.0
162	278	14.1	362	2	A56741	G protein-coupled	232	241	11.9
163	277	14.1	362	2	S68207	melatonin receptor	233	241	11.8
164	281	14.3	404	2	C42009	neurokinin 2 recep	234	241	11.8
165	277	14.1	384	2	A42685	cholecystokinin rec	235	241	11.8
166	276	14.0	402	2	I56595	neurokinin 2 recep	236	241	11.8
167	276	14.0	443	2	A40470	G protein-coupled	237	241	11.7
168	274	13.9	613	2	S70520	melatonin receptor	238	240	11.7
169	274	13.9	398	1	JQ1059	neurokinin 2 recep	239	240	11.7
170	274	13.9	427	2	S50150	gastric CCK-A rece	240	240	11.7
171	273	13.9	361	2	JC5653	G protein-coupled	241	240	11.7
172	270	13.7	358	2	T30999	TB-1-related recept	242	239	11.6
173	270	13.7	384	2	A45490	Glucocorticoid-ind	243	239	11.6
174	270	13.7	391	2	T32714	melatonin receptor	244	239	11.6
175	268	13.6	384	2	A39003	neurokinin 1 recep	245	228	11.6

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OM protein - protein search, using SW model

Run on: March 29, 2006, 13:38:04 ; Search time 188 Seconds

(without alignment)

874.083 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970

Sequence: 1 MLSTSRSPTRNTNNSGEV.....GKGRSTGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0⁺

Maximum Match 99.9999%⁺

Listing first 1045 summaries

Database : A_GenSeq_21:⁺

1: GenSeqP1980s:^{*}

2: GenSeqP1990s:^{*}

3: GenSeqP2000s:^{*}

4: GenSeqP2001s:^{*}

5: GenSeqP2002s:^{*}

6: GenSeqP2003s:^{*}

7: GenSeqP2003s:^{*}

8: GenSeqP2004s:^{*}

9: GenSeqP2005s:^{*}

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1823	92.5	344	5	ABG92881	Abg92881 Class I r	
2	1823	92.5	344	6	ABU61555	Abu61555 Human mon	
3	1823	92.5	344	7	ADP72219	Adp72219 Human G-P	
4	1823	92.5	344	8	ADP86217	Adp86217 Human MCP	
5	1727.5	87.7	329	4	AAB46559	Aab46559 Human MCP	
6	1727.5	87.7	329	5	ABP81055	Abp81055 Human MCP	
7	1727.5	87.7	329	8	ADR16266	Adr16266 Human MCP	
8	1651.5	83.8	360	2	AAR79166	Aar79166 Human mon	
9	1651.5	83.8	360	3	AAW35333	Aaw35333 Human mon	
10	1651.5	83.8	360	4	AAG80108	Aag80108 Human CCR	
11	1651.5	83.8	360	4	AAU07614	Aau07614 Human wil	
12	1651.5	83.8	360	6	ABP97725	Abp97725 Human ac1	
13	1651.5	83.8	360	6	ABP81987	Abp81987 Human C-C	
14	1651.5	83.8	360	8	ADM67225	Adm67225 Human ad1	
15	1651.5	83.8	360	8	ADL8231	Adl8231 Human PRO	
16	1651.5	83.8	360	9	ADY15868	Ady15868 PRO polyp	
17	1650.5	83.8	360	4	AAU07613	Aau07613 Human CCR	
18	1645.5	83.8	360	4	ABP6340	Abp6340 Non-endog	
19	1589.5	80.7	347	7	ADF56627	Adf56627 Partial h	
20	1589.5	80.7	347	9	ADW15156	Adw15156 Human mon	
21	1582.5	80.3	384	9	AEB22130	Aeb22130 Human che	
22	1332.5	67.6	373	8	ADM67224	Adm67224 Murine ad	
23	1332.5	67.6	373	8	ADO29222	Ado29222 Mouse GPC	
24	1332.5	67.6	373	8	ADP74040	Adp74040 Murine CC	

98	967.5	49.1	355	4	AAG80106	Human	CCR	Aag80106	Human	CCR	ADY20385	PRO polyp	171	831.5	42.2	360	9							
99	967.5	49.1	355	5	AD51688	Human	CCR	Abi09082	Human	che	AD211715		172	831.5	42.2	360	9							
100	967.5	49.1	355	6	ABU05082	Human	che	Abp97724	Amino	aci	AD252555	Human	CC	AD252555		173	831.5	42.2	360	9				
101	967.5	49.1	355	6	ABP97724	Human	C-C	Abp97724	Amino	aci	Aea33220	Human	CC	Aea33220		174	831.5	42.2	360	9				
102	967.5	49.1	355	6	ABP81790	Human	C-C	Abp81790	Human	C-C	ABP11966		175	831.5	42.2	360	9							
103	967.5	49.1	355	7	ADF76506	Novel	hum	Adi76506	Novel	hum	AAR9274	Chemokine	176	828.5	42.1	360	4							
104	967.5	49.1	355	7	ADO16838	CCR1	amino	Ado16838	CCR1	amino	ABP97727	Amino	aci	ABP97727		177	828.5	42.1	360	6				
105	967.5	49.1	355	8	ADo29219	Human	GPC	Ado29219	Human	GPC	ABP1684	G	protein	ABP1684		178	794.5	40.3	383	5				
106	967.5	49.1	355	8	ADO19490	Human	PRO	Ado19490	Human	PRO	Aao22930	3.56	Human	CC	Aao22930	3.56	5	AAc80115		179	731	37.1	356	5
107	967.5	49.1	355	8	ADO19492	Human	PRO	Ado19492	Human	PRO	Ado29711	Mouse	GPC	Ado29711		180	731	37.1	356	8				
108	967.5	49.1	355	8	ADQ1524	Human	sof	Adq1524	Human	sof	Aau80233	Human	che	Aau80233		181	730	37.1	355	5				
109	967.5	49.1	355	8	ADP88568	Human	che	Adp88568	Human	che	Aau80233	Human	che	Aau80233		182	723	36.7	355	2				
110	967.5	49.1	355	8	ADP88570	Human	mac	Adp88570	Human	mac	Aau80233	Human	che	Aau80233		183	723	36.7	355	2				
111	967.5	49.1	355	8	ADQ67846	Human	che	Adq67846	Human	che	Aaw49807	Human	G-P	Aaw49807		184	723	36.7	355	2				
112	967.5	49.1	355	8	ADR14581	Human	NF-	Adr14581	Human	NF-	Aaw7868	Human	CC	Aaw7868		185	723	36.7	355	4				
113	967.5	49.1	355	9	ADY15488	Human	PRO	Ady15488	Human	PRO	Ado29711	Mouse	GPC	Ado29711		186	723	36.7	355	5				
114	967.5	49.1	355	9	ADY15652	Human	PRO	Ady15652	Human	PRO	Ado29233	Human	GPC	Ado29233		187	723	36.7	355	8				
115	967.5	49.1	355	9	ADY15486	Human	PRO	Ady15486	Human	PRO	Abp97731	Amino	aci	Abp97731		188	723	36.7	355	6				
116	967.5	49.1	355	9	ADZ11712	Human	che	Adz11712	Human	che	Adw15155	Human	G-P	Adw15155		189	723	36.7	355	6				
117	967.5	49.1	355	9	Aea23748	Human	PRO	Aea23748	Human	PRO	Abp81794	Human	C-C	Abp81794		190	723	36.7	355	6				
118	967.5	49.1	355	9	AEA23621	Human	PRO	Aea23621	Human	PRO	Adf56626	Human	G-P	Adf56626		191	723	36.7	355	8				
119	967.5	49.1	355	9	AEB22127	Human	che	Adb22127	Human	che	Aad30384	Human	che	Aad30384		192	723	36.7	355	8				
120	967.5	49.1	355	9	ADQ2924	Human	GPC	Adq2924	Human	GPC	Ado43139	Human	che	Ado43139		193	723	36.7	355	8				
121	967.5	49.1	355	9	AAW5179	Rat	C-C	Aaw5179	Rat	C-C	Ado29233	Human	GPC	Ado29233		194	723	36.7	355	9				
122	967.5	49.1	355	9	ADD45360	Rat	Prote	Add45360	Rat	Prote	Aar53748	Seven	tra	Aar53748		195	723	36.7	355	6				
123	967.5	49.1	355	9	ADZ58687	Mouse	CCR	Adz58687	Mouse	CCR	Aab77933	Human	V28	Aab77933		196	718	36.7	355	4				
124	899.5	45.7	355	8	ADQ2920	Mouse	GPC	Adq2920	Mouse	GPC	Aab56639	Human	7TM	Aab56639		197	717	36.4	355	2				
125	899.5	45.7	355	8	AEB22127	Human	che	Adb22127	Human	che	Ado29234	Mouse	GPC	Ado29234		198	708.5	36.0	353	8				
126	898.5	45.6	355	9	ABE22128	Human	che	Adb22128	Human	che	Adh10684	Rat	Sprag	Adh10684		199	704.5	35.8	354	8				
127	897.5	45.6	355	9	AEB22128	Human	C-C	Aeb22128	Human	C-C	Aar53748	Seven	tra	Aar53748		200	698	35.4	355	2				
128	890.5	45.6	355	9	AAW03376	Human	ova	Aaw03376	Human	ova	Abp97732	Human	CX3	Abp97732		201	698	35.4	355	2				
129	890.5	45.2	355	9	AAW01000	Human	C-C	Aaw01000	Human	C-C	Aab82786	Human	CX3	Aab82786		202	698	35.4	355	2				
130	890.5	45.2	355	9	ABD07240	Human	CC	Abd07240	Human	CC	Aau91235	Human	T	Aau91235		203	698	35.4	355	3				
131	890.5	45.2	355	9	ABD07733	Human	C-C	Abd07733	Human	C-C	Aab21692	Human	7TM	Aab21692		204	698	35.4	355	3				
132	890.5	45.2	355	9	ABG7634	Human	C-C	Abg7634	Human	C-C	Aar51353	Human	fra	Aar51353		205	698	35.4	355	4				
133	886.5	45.0	355	5	ABJ03698	Human	che	Aae15320	Human	che	Abp97732	Amino	aci	Abp97732		206	698	35.4	355	6				
134	886.5	45.0	355	5	ABU09084	Human	che	Abu09084	Human	che	Aab81882	Human	PRO	Aab81882		207	698	35.4	355	6				
135	886.5	45.0	355	5	ABW03377	Human	che	Aaw03377	Human	che	Adc22649	Human	PRO	Adc22649		208	698	35.4	355	5				
136	886.5	45.0	355	5	AAW31850	Human	eos	Aaw31850	Human	eos	Aau91234	Human	ser	Aau91234		209	698	35.4	355	5				
137	886.5	45.0	355	5	AAW51745	Human	C-C	Aaw51745	Human	C-C	Abp58524	Human	che	Abp58524		210	698	35.4	355	6				
138	886.5	45.0	355	4	AAG80109	Human	CCR	Aag80109	Human	CCR	Aro29513	Human	sof	Aro29513		211	698	35.4	355	4				
139	886.5	45.0	355	4	AAE15320	Human	che	Aae15320	Human	che	Abp97732	Amino	aci	Abp97732		212	698	35.4	355	6				
140	886.5	45.0	355	4	ABU09084	Human	che	Abu09084	Human	che	Aab81882	Human	PRO	Aab81882		213	698	35.4	355	6				
141	886.5	45.0	355	4	ABP97726	Amino	aci	Abp97726	Amino	aci	Adp54585	Human	PRO	Adp54585		214	698	35.4	355	7				
142	886.5	45.0	355	4	ABU09084	Human	che	Abu09084	Human	che	Adh14122	Human	ser	Adh14122		215	698	35.4	355	7				
143	886.5	45.0	355	4	ABD03343	Human	che	Adc03343	Human	che	Adp39421	Human	myo	Adp39421		216	698	35.4	355	8				
144	886.5	45.0	355	4	ABD02923	Human	GPC	Adb2923	Human	GPC	Ado29269	Human	GPC	Ado29269		217	698	35.4	355	9				
145	886.5	44.7	355	4	ADQ67848	Human	C-C	Adq67848	Human	C-C	Adq18141	Human	myo	Adq18141		218	698	35.4	355	8				
146	886.5	44.7	355	4	ADT90849	Human	CCR	Adt90849	Human	CCR	Adp56020	Human	PRO	Adp56020		219	698	35.4	355	8				
147	886.5	44.7	355	4	ADU47728	Human	che	Adu47728	Human	che	Adp56020	Human	PRO	Adp56020		220	698	35.4	355	7				
148	886.5	44.7	355	4	ADY15934	Human	PRO	Ady15934	Human	PRO	Adp39421	Human	myo	Adp39421		221	698	35.4	355	8				
149	886.5	45.0	355	9	ADY19620	Human	CCR	Aad1044	Human	CCR	Ado29270	Mouse	GPC	Ado29270		222	698	35.4	355	8				
150	886.5	45.0	355	9	ADZ11714	Human	che	Adz11714	Human	che	Aab957673	Amino	aci	Aab957673		223	693	35.2	355	7				
151	881.5	44.7	355	9	ADW03378	CC-chemok	C-C	Aaw03378	CC-chemok	C-C	Adc22751	Human	G-P	Adc22751		224	693	35.2	355	7				
152	882.5	43.8	355	2	AAW51746	Human	CCR	Aaw51746	Human	CCR	Adm35892	Fusion	Pr	Adm35892		225	693	35.2	355	7				
153	881.5	42.3	360	8	ADC10142	Human	CCR	Adc10142	Human	CCR	Adh14224	Human	PRO	Adh14224		226	692	35.1	344	9				
154	881.5	42.2	360	3	AAB07498	A	human	Adb107498	A	human	Adb107498	Mouse	CX3	Adb107498		227	692	35.1	344	8				
155	863	43.8	360	4	AAG80110	Human	CCR	Aag80110	Human	CCR	Aab80110	Human	CCR	Aab80110		228	692	35.1	344	8				
156	862.5	43.8	360	4	AAG67673	Human	che	Aag67673	Human	che	Aab957673	Amino	aci	Aab957673		229	693	35.1	344	8				
157	862.5	43.8	360	4	AAB40283	Human	am1	Abp40283	Human	am1	Abp40283	Human	am1	Abp40283		230	693	35.2	344	8				
158	862	43.8	360	6	ABU09085	Human	che	Abu09085	Human	che	Abp81792	Human	C-C	Abp81792		231	693	35.2	344	2				
159	861.5	42.3	360	8	ADP81792	Human	PRO	Adp81792	Human	PRO	Abp81792	Human	C-C	Abp81792		232	692	35.1	344	9				
160	861.5	42.2	360	3	AAB07498	A	human	Adb107498	A	human	Adb107498	Mouse	CX3	Adb107498		233	692	35.1	344	8				
161	861.5	42.1	360	4	AAG80110	Human	CCR	Aag80110	Human	CCR	Aab80110	Human	CCR	Aab80110		234	692	35.1						

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7	Sequence 546, App
OM protein - protein search, using sw model.	Sequence 2, App1	Sequence 2, App1
Run on: March 29, 2006, 13:58:15 ; Search time 25 Seconds (without alignment)	Sequence 57, App	Sequence 921, App
Scoring table: BLOSUM62	Sequence 2, App1	Sequence 2, App1
Title: US-10-791-592-2	Sequence 712, App	Sequence 712, App
Perfect score: 1970	Sequence 716, App	Sequence 716, App
Sequence: 1 MLSTRSRFRNTNNSGEEV.....GKGRSIGRAPEASTQDKEGA 374	Sequence 65, App	Sequence 65, App
Total number of hits satisfying chosen parameters: 180807	Sequence 711, App	Sequence 711, App
Minimum DB seq length: 0	Sequence 714, App	Sequence 714, App
Maximum DB seq length: 2000000000	Sequence 715, App	Sequence 715, App
Post-processing: Minimum Match 0\$	Sequence 248, App	Sequence 248, App
Maximum Match 99.9999%	Sequence 327, App	Sequence 327, App
Listing first 1045 summaries	Sequence 346, App	Sequence 346, App
Database : Published Applications AA_New:*	Sequence 83, App1	Sequence 83, App1
1: /SDSS7/ptodata/2/_pubpas/US08_NEW_PUB_pep:*	Sequence 52, App1	Sequence 52, App1
2: /SDSS5/ptodata/2/_pubpas/_US06_NEW_PUB_pep:*	Sequence 225, App	Sequence 225, App
3: /SDSS5/ptodata/2/_pubpas/_US07_NEW_PUB_pep:*	Sequence 231, App	Sequence 231, App
4: /SDSS5/ptodata/2/_pubpas/_US05_NEW_PUB_pep:*	Sequence 27, App1	Sequence 27, App1
5: /SDSS5/ptodata/2/_pubpas/_US09_NEW_PUB_pep:*	Sequence 79, App1	Sequence 79, App1
6: /SDSS5/ptodata/2/_pubpas/_US10_NEW_PUB_pep:*	Sequence 81, App1	Sequence 81, App1
7: /SDSS5/ptodata/2/_pubpas/_US11_NEW_PUB_pep:*	Sequence 29, App1	Sequence 29, App1
8: /SDSS5/ptodata/2/_pubpas/_US60_NEW_PUB_pep:*	Sequence 838, App	Sequence 838, App
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Sequence 77, App1	Sequence 77, App1
SUMMARIES	Sequence 17, App1	Sequence 17, App1
Result No.	Score	Query Match Length DB ID Description
1	1224	62.1 352 6 US-10-995-561-523 Sequence 523, App
2	1224	62.1 352 7 US-11-068-686-2 Sequence 2, App1
3	1224	62.1 352 7 US-11-068-686-20 Sequence 20, App1
4	1224	62.1 352 7 US-11-127-877-61 Sequence 61, App1
5	897	45.6 355 7 US-11-216-610-2 Sequence 2, App1
6	886	45.0 355 7 US-11-068-686-4 Sequence 4, App1
7	698	35.4 355 7 US-11-127-877-64 Sequence 64, App1
8	886	45.0 355 7 US-11-216-610-4 Sequence 4, App1
9	862	43.8 355 7 US-11-216-610-6 Sequence 6, App1
10	831.5	42.2 360 6 US-10-995-561-522 Sequence 36, App1
11	831.5	42.2 360 7 US-11-144-731-0 Sequence 1, App1
12	831.5	42.2 360 7 US-11-262-284-24 Sequence 34, App1
13	698	35.4 355 6 US-10-995-561-636 Sequence 63, App1
14	698	35.4 362 6 US-10-995-561-637 Sequence 637, App1
15	696	35.3 216 6 US-10-995-561-522 Sequence 522, App1
16	45.5	32.8 344 6 US-10-995-561-524 Sequence 52, App1
17	45.5	32.8 344 6 US-10-995-561-525 Sequence 525, App1
18	569	28.9 357 7 US-11-261-135-2 Sequence 62, App1
19	545.5	28.1 374 7 US-11-127-877-62 Sequence 62, App1
20	541.5	27.5 353 7 US-11-017-058-9 Sequence 9, App1
21	535	27.2 351 7 US-11-122-849-2 Sequence 2, App1
22	534.5	27.1 368 6 US-10-920-055-6 Sequence 6, App1
23	534.5	27.1 415 7 US-11-017-058-2 Sequence 2, App1
24	528	26.8 352 7 US-11-028-922A1 Sequence 1, App1
25	526	26.7 367 6 US-10-920-055-7 Sequence 7, App1

99	267	13.6	430	6	US-10-992-577-8	Sequence 8, App1	Sequence 30, App1	7	US-11-174-819-30
100	267	13.6	430	6	US-10-508-892-2	Sequence 2, App1	Sequence 112, App1	348	US-11-174-819-54
	267	13.6	430	7	US-11-223-294-54	Sequence 54, App1	Sequence 112, App1	203	US-10-980-308-112
102	265.5	13.5	384	7	US-11-127-877-44	Sequence 41, App1	Sequence 22, App1	173	US-11-174-819-77
103	361.5	13.3	340	6	US-10-980-388-117	Sequence 117, App1	Sequence 47, App1	174	US-11-174-751-22
104	361.5	13.3	340	7	US-11-127-877-53	Sequence 53, App1	Sequence 45, App1	175	US-10-877-346-47
105	257	13.0	356	7	US-11-218-881-27	Sequence 27, App1	Sequence 45, App1	176	US-11-174-816-45
106	252	12.8	482	7	US-11-169-976-2	Sequence 2, App1	Sequence 28, App1	177	US-11-174-819-28
107	252	12.8	482	7	US-11-218-281-10	Sequence 30, App1	Sequence 29, App1	178	US-11-174-819-27
108	249.5	12.7	188	7	US-11-206-587-32	Sequence 32, App1	Sequence 30, App1	179	US-10-987-816-43
109	248.5	12.6	309	6	US-10-537-002-9	Sequence 9, App1	Sequence 31, App1	180	US-11-174-819-11
110	248.5	12.6	394	6	US-10-537-002-10	Sequence 10, App1	Sequence 32, App1	181	US-11-174-816-5
111	247.5	12.6	342	7	US-11-151-482-1	Sequence 1, App1	Sequence 32, App1	182	US-11-174-819-86
112	247.5	12.6	393	7	US-11-073-420-32	Sequence 32, App1	Sequence 32, App1	183	US-11-174-816-49
113	244.5	12.4	120	6	US-10-055-877-179	Sequence 179, App1	Sequence 179, App1	184	US-11-174-819-15
114	244.5	12.4	412	7	US-11-170-153-8	Sequence 8, App1	Sequence 8, App1	185	US-11-174-816-42
115	244.5	12.4	412	7	US-11-170-166-8	Sequence 8, App1	Sequence 8, App1	186	US-10-987-856-2
116	244.5	12.4	412	7	US-11-170-351-8	Sequence 8, App1	Sequence 8, App1	187	US-11-174-816-5
117	244.5	12.4	415	7	US-11-170-153-6	Sequence 6, App1	Sequence 6, App1	188	US-11-174-816-7
118	244.5	12.4	415	7	US-11-170-166-6	Sequence 6, App1	Sequence 6, App1	189	US-11-174-819-56
119	244.5	12.4	415	7	US-11-170-351-6	Sequence 6, App1	Sequence 6, App1	190	US-11-127-877-66
120	243.5	12.4	403	6	US-10-503-511-2	Sequence 2, App1	Sequence 2, App1	191	US-10-055-877-177
121	241.5	12.3	412	7	US-11-170-153-4	Sequence 4, App1	Sequence 4, App1	192	US-11-174-816-58
122	241.5	12.3	412	7	US-11-170-166-4	Sequence 4, App1	Sequence 4, App1	193	US-11-174-819-15
123	241.5	12.3	412	7	US-11-170-351-4	Sequence 2, App1	Sequence 2, App1	194	US-11-166-412-67
124	241.5	12.3	415	7	US-11-170-153-2	Sequence 2, App1	Sequence 2, App1	195	US-11-174-816-9
125	241.5	12.3	415	7	US-11-170-166-2	Sequence 2, App1	Sequence 2, App1	196	US-10-875-716-9
126	241.5	12.3	415	7	US-11-170-351-2	Sequence 2, App1	Sequence 2, App1	197	US-11-174-816-64
127	241.5	12.3	415	7	US-11-127-877-45	Sequence 2, App1	Sequence 2, App1	198	US-11-174-819-58
128	241	12.2	414	6	US-10-515-966-2	Sequence 30, App1	Sequence 30, App1	199	US-10-055-877-178
129	240	12.2	393	7	US-11-073-420-30	Sequence 3, App1	Sequence 3, App1	200	US-11-174-816-42
130	239	12.2	342	7	US-11-151-482-3	Sequence 2, App1	Sequence 2, App1	201	US-11-174-819-3
131	239	12.1	407	7	US-11-127-877-16	Sequence 56, App1	Sequence 56, App1	202	US-11-174-819-2
132	238	12.1	458	6	US-10-877-346-51	Sequence 51, App1	Sequence 51, App1	203	US-11-174-751-6
133	236.5	12.0	395	7	US-11-218-281-39	Sequence 17, App1	Sequence 17, App1	204	US-11-165-02-3
134	232	11.8	394	7	US-11-183-615-17	Sequence 34, App1	Sequence 34, App1	205	US-10-875-716-2
135	231.5	11.8	442	7	US-11-100-640-34	Sequence 2, App1	Sequence 2, App1	206	US-10-877-855-4
136	229	11.6	384	7	US-11-073-420-3	Sequence 4, App1	Sequence 4, App1	207	US-11-183-615-7
137	228.5	11.6	384	7	US-11-127-877-50	Sequence 7, App1	Sequence 7, App1	208	US-10-877-346-50
138	227	11.5	384	7	US-11-073-420-7	Sequence 17, App1	Sequence 17, App1	209	US-11-174-819-9
139	227	11.4	375	6	US-10-987-856-17	Sequence 18, App1	Sequence 18, App1	210	US-11-174-819-13
140	223	11.3	384	7	US-11-073-420-8	Sequence 96, App1	Sequence 96, App1	211	US-10-627-633-6
141	219	11.1	475	6	US-10-877-346-48	Sequence 48, App1	Sequence 48, App1	212	US-11-174-816-55
142	218	11.1	429	7	US-11-127-877-51	Sequence 51, App1	Sequence 51, App1	213	US-11-174-816-59
143	218.5	11.1	466	7	US-11-127-877-50	Sequence 50, App1	Sequence 50, App1	214	US-11-174-816-52
144	218	11.1	384	7	US-11-174-816-60	Sequence 60, App1	Sequence 60, App1	215	US-11-174-816-44
145	218	11.1	344	7	US-11-174-819-79	Sequence 79, App1	Sequence 79, App1	216	US-11-174-819-24
146	218	11.1	389	6	US-10-513-118-2	Sequence 2, App1	Sequence 2, App1	217	US-11-174-819-24
147	216	11.0	358	6	US-10-980-388-96	Sequence 116, App1	Sequence 116, App1	218	US-11-174-816-55
148	216	11.0	389	6	US-10-980-388-116	Sequence 115, App1	Sequence 115, App1	219	US-11-174-816-57
149	214	10.9	337	6	US-10-980-388-115	Sequence 49, App1	Sequence 49, App1	220	US-11-174-816-59
150	213.5	10.8	457	6	US-10-877-346-49	Sequence 55, App1	Sequence 55, App1	221	US-11-174-816-61
151	213	10.7	345	7	US-11-174-816-15	Sequence 15, App1	Sequence 15, App1	222	US-11-174-816-63
152	211.5	10.7	345	7	US-11-174-819-70	Sequence 70, App1	Sequence 70, App1	223	US-11-174-816-65
153	211	10.7	344	7	US-11-174-816-61	Sequence 61, App1	Sequence 61, App1	224	US-11-174-816-66
154	206.5	10.5	342	7	US-11-174-819-71	Sequence 80, App1	Sequence 80, App1	225	US-11-174-816-67
155	211	10.7	344	7	US-11-174-751-16	Sequence 16, App1	Sequence 16, App1	226	US-11-174-816-69
156	208.5	10.6	339	7	US-11-174-816-55	Sequence 55, App1	Sequence 55, App1	227	US-11-174-816-71
157	206.5	10.6	339	7	US-11-174-819-32	Sequence 15, App1	Sequence 15, App1	228	US-11-127-877-48
158	205.5	10.4	345	7	US-10-980-388-118	Sequence 74, App1	Sequence 74, App1	229	US-11-174-816-51
159	204.5	10.4	342	6	US-10-995-561-01	Sequence 118, App1	Sequence 118, App1	230	US-11-174-816-52
160	204.5	10.4	339	7	US-11-174-816-40	Sequence 18, App1	Sequence 18, App1	231	US-11-174-816-53
161	206	10.5	344	7	US-11-174-816-62	Sequence 71, App1	Sequence 71, App1	232	US-11-174-816-54
162	206	10.5	344	7	US-11-174-816-81	Sequence 47, App1	Sequence 47, App1	233	US-11-174-816-55
163	205.5	10.4	371	6	US-10-501-035-242	Sequence 242, App1	Sequence 242, App1	234	US-11-174-816-56
164	205	10.4	471	7	US-10-995-816-01	Sequence 90, App1	Sequence 90, App1	235	US-11-174-816-57
165	204.5	10.4	339	7	US-11-174-816-40	Sequence 5, App1	Sequence 5, App1	236	US-11-174-816-58
166	204.5	10.4	344	7	US-11-174-819-55	Sequence 47, App1	Sequence 47, App1	237	US-11-174-816-59
167	204.5	10.4	344	7	US-11-174-816-62	Sequence 81, App1	Sequence 81, App1	238	US-11-174-816-60
168	204.5	10.4	344	7	US-11-174-819-32	Sequence 74, App1	Sequence 74, App1	239	US-11-174-816-61
169	204.5	10.4	358	7	US-11-174-816-68	Sequence 68, App1	Sequence 68, App1	240	US-11-174-816-62
170	204.5	10.4	358	7	US-11-174-819-37	Sequence 87, App1	Sequence 87, App1	241	US-11-127-877-54
171	203	10.3	344	7	US-11-174-816-46	Sequence 46, App1	Sequence 46, App1	242	US-11-124-368A-183

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OM protein - protein search, using sw model

Run on: March 29, 2006, 13:57:19 ; Search time 167 Seconds

(without alignments)

935.738 Million cell updates/sec

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867555

Post-processing: Minimum Match 0*

Minimum Match 99.9999%ⁱⁱ

Maximum Match 99.9999%ⁱⁱ

Listing first 1045 summaries

Database : Published Applications AA_Main.*

1: /cgn2_6_ptodata/1_pubpba/US07_PUCOMB_pep:*

2: /cgn2_6_ptodata/1_pubpba/US08_PUCOMB_pep:*

3: /cgn2_6_ptodata/1_pubpba/US09_PUCOMB_pep:*

4: /cgn2_6_ptodata/1_pubpba/US10_PUCOMB_pep:*

5: /cgn2_6_ptodata/1_pubpba/US10B_PUCOMB_pep:*

6: /cgn2_6_ptodata/1_pubpba/US11_PUCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1823	92.5	344	US-09-779-879A-9
2	1823	92.5	344	US-09-779-880A-9
3	1823	92.5	344	US-10-232-686-9
4	1823	92.5	344	US-10-067-800-9
5	1823	92.5	344	US-10-135-839-9
6	1823	92.5	344	US-10-994-679-9
7	1727	87.7	329	US-09-725-285-9
8	1727	87.7	329	US-09-195-662A-9
9	1727	87.7	329	US-09-339-912A-9
10	1727	87.7	329	US-09-502-783A-9
11	1727	87.7	329	US-10-791-905-9
12	1727	87.7	329	US-10-127-644-9
13	1651	83.8	360	US-09-131-827A-2
14	1651	83.8	360	US-10-225-567A-460
15	1651	83.8	360	US-10-164-649-610
16	1651	83.8	360	US-10-239-423-64
17	1651	83.8	360	US-10-439-845-8
18	1651	83.8	360	US-10-741-601-285
19	1651	83.8	360	US-10-741-601-286
20	1651	83.8	360	US-10-791-592-4
21	1651	83.8	360	US-10-166-4
22	1651	83.8	360	US-10-700-313-8
23	1651	83.8	360	US-10-486-471-4
24	1651	83.8	360	US-10-846-185-8
25	1651	83.8	360	US-10-988-267-8
26	1651	83.8	359	US-10-988-267-24
27	1650.5	83.8	360	US-09-131-827A-20

28	1645.5	83.5	360	US-09-938-719-7
29	1645.5	83.5	360	US-09-938-703-7
30	1645.5	83.5	360	US-10-661-798-3
31	1645.5	83.5	360	US-10-612-791-7
32	1645.5	83.5	360	US-10-925-095-473
33	1645.5	83.5	360	US-10-164-649-51
34	1645.5	82.0	360	US-10-151-274-5
35	1614.5	80.7	347	US-09-104-792-3
36	1589.5	80.7	347	US-10-176-178-3
37	1589.5	80.7	347	US-10-893-996-3
38	1589.5	80.7	347	US-10-893-512-14
39	1582.5	80.3	384	US-10-799-736-14
40	1582.5	80.3	384	US-10-151-274-5
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87	1219	61.9	352	US-10-844-185-2
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89	1218	61.8	352	US-09-826-509-477
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95	1215	61.7	352	US-10-099-679-2
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125	940.5	47.7	355	3	US-10-846-226-9	Sequence 9, App1	Sequence 56, App1
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127	940.5	47.7	355	4	US-10-661-798-9	Sequence 9, App1	Sequence 56, App1
128	940.5	47.7	355	4	US-10-612-791-9	Sequence 9, App1	Sequence 56, App1
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132	899.5	45.7	355	3	US-09-931-319A-13	Sequence 13, App1	Sequence 1085, App1
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135	898.5	45.6	379	3	US-10-799-736-12	Sequence 12, App1	Sequence 130, App1
136	897.5	45.6	355	4	US-10-283-028-2	Sequence 2, App1	Sequence 249, App1
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149	886.5	45.0	355	5	US-10-767-521-1	Sequence 1, App1	Sequence 6, App1
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155	881.5	44.7	355	5	US-10-925-095-475	Sequence 475, App1	Sequence 16, App1
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157	875	44.4	356	4	US-10-491-997-02	Sequence 102, App1	Sequence 16, App1
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159	862.5	43.8	355	4	US-09-828-028-6	Sequence 6, App1	Sequence 16, App1
160	858.5	43.6	355	3	US-09-938-719-8	Sequence 8, App1	Sequence 16, App1
161	858.5	43.6	355	3	US-09-939-226-8	Sequence 8, App1	Sequence 16, App1
162	858.5	43.6	355	3	US-09-938-703-8	Sequence 8, App1	Sequence 16, App1
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171	831.5	42.2	360	4	US-10-164-649-55	Sequence 55, App1	Sequence 16, App1
172	831.5	42.2	360	4	US-10-145-452-84	Sequence 48, App1	Sequence 4, App1
173	831.5	42.2	360	4	US-10-239-423-66	Sequence 66, App1	Sequence 396, App1

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OM protein - protein search, using SW model

Run on: March 29, 2006, 13:45:59 ; Search time 48 Seconds

(without alignments) 644.181 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 1970

Sequence: 1 MLLSRSRPIRNTNNSGEV.....GKGRSIGRAPEASIQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572054

Post-processing: Minimum Match 0% ; Maximum Match 99.999%

Listing first 1045 summaries

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMBO.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMBO.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMBO.pep:*
- 4: /cgn2_6/ptodata/1/iaa/FACTUS_COMBO.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RCB_COMBO.pep:*
- 6: /cgn2_6/ptodata/1/iaa/haGKfleles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1823	92.5	344 2 US-08-466-343D-9	Sequence 9, Appli
2	1823	92.5	344 2 US-09-502-784A-9	Sequence 9, Appli
3	1727.5	87.7	329 2 US-09-502-783A-9	Sequence 9, Appli
4	1727.5	87.7	329 2 US-09-339-912A-9	Sequence 9, Appli
5	1727.5	87.7	329 2 US-09-195-662A-9	Sequence 9, Appli
6	1651.5	83.8	360 1 US-08-450-393A-4	Sequence 4, Appli
7	1651.5	83.8	360 2 US-08-446-669-4	Sequence 4, Appli
8	1651.5	83.8	360 2 US-09-045-583-50	Sequence 50, Appli
9	1645.5	83.8	360 2 US-09-534-185-50	Sequence 50, Appli
10	1651.5	83.8	360 2 US-09-131-827A-2	Sequence 2, Appli
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15	1645.5	83.5	360 2 US-08-833-752-7	Sequence 7, Appli
16	1645.5	83.5	360 2 US-09-938-719-7	Sequence 7, Appli
17	1645.5	83.5	360 2 US-09-939-226B-7	Sequence 7, Appli
18	1645.5	83.5	360 2 US-09-826-509-473	Sequence 473, Appli
19	1645.5	83.5	360 2 US-09-938-703B-7	Sequence 7, Appli
20	1614.5	82.0	360 2 US-09-045-583-51	Sequence 51, Appli
21	1614.5	82.0	360 2 US-09-534-185-51	Sequence 51, Appli
22	1589.5	80.7	347 1 US-08-461-244-3	Sequence 3, Appli
23	1236	62.7	352 2 US-09-517-605-5	Sequence 5, Appli
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26	1230	62.4	352 2 US-09-534-185-52	Sequence 52, Appli
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37	1224	62.1	US-09-276-227-2	Sequence 2, Appli
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54	967.5	49.1	US-09-960-547-1	Sequence 5, Appli
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112	694	35.2	184	2	US-09-938-703B-6	Sequence 4, App1	Sequence 2, App1
113	694	35.2	215	2	US-09-087-232A-17	Sequence 17, App1	Sequence 2, App1
114	694	35.2	215	2	US-08-833-752-6	Sequence 6, App1	Sequence 174, App1
115	694	35.2	215	2	US-09-938-719-6	Sequence 6, App1	Sequence 2, App1
116	694	35.2	215	2	US-09-939-226B-6	Sequence 6, App1	Sequence 2, App1
117	694	35.2	215	2	US-09-938-703B-6	Sequence 6, App1	Sequence 2, App1
118	694	35.2	215	2	US-09-928-703B-18	Sequence 18, App1	Sequence 2, App1
119	694	35.2	215	2	US-09-170-496D-232	Sequence 17, App1	Sequence 2, App1
120	693	35.2	215	2	US-08-681-192-2	Sequence 2, App1	Sequence 1, App1
121	645	32.8	344	2	US-09-938-719-2	Sequence 6, App1	Sequence 1, App1
122	644	32.7	356	2	US-10-039-659A-12	Sequence 12, App1	Sequence 2, App1
123	588	29.8	384	2	US-09-045-583-2	Sequence 6, App1	Sequence 4, App1
124	588	29.8	384	2	US-09-534-185-2	Sequence 2, App1	Sequence 4, App1
125	584	29.6	358	1	US-08-153-848-19	Sequence 6, App1	Sequence 4, App1
126	584	29.6	358	2	US-09-299-843A-19	Sequence 18, App1	Sequence 4, App1
127	584	29.6	358	2	US-09-088-337B-19	Sequence 19, App1	Sequence 4, App1
128	584	29.6	358	4	PCT-US93-11153-19	Sequence 19, App1	Sequence 4, App1
129	584	29.6	378	1	US-08-153-848-7	Sequence 15, App1	Sequence 4, App1
130	584	29.6	378	1	US-09-299-843A-15	Sequence 15, App1	Sequence 4, App1
131	584	29.6	378	2	US-09-088-337B-7	Sequence 1, App1	Sequence 4, App1
132	584	29.6	378	2	US-09-251-545-1	Sequence 19, App1	Sequence 4, App1
133	584	29.6	378	2	US-09-088-337B-15	Sequence 15, App1	Sequence 4, App1
134	584	29.6	378	2	US-09-170-496D-74	Sequence 19, App1	Sequence 4, App1
135	584	29.6	378	4	PCT-US93-11153-15	Sequence 15, App1	Sequence 4, App1
136	584	29.6	410	1	US-08-153-848-7	Sequence 7, App1	Sequence 4, App1
137	584	29.6	410	2	US-09-299-843A-7	Sequence 7, App1	Sequence 4, App1
138	584	29.6	410	4	PCT-US93-11153-7	Sequence 7, App1	Sequence 4, App1
139	580	29.4	378	2	US-09-170-496D-74	Sequence 74, App1	Sequence 46, App1
140	580	29.4	378	4	PCT-US93-11153-15	Sequence 15, App1	Sequence 46, App1
141	579	29.4	378	2	US-09-170-496D-204	Sequence 7, App1	Sequence 46, App1
142	575	29.2	378	2	US-09-299-843A-66	Sequence 66, App1	Sequence 485, App1
143	575	29.2	378	2	US-09-088-337B-66	Sequence 66, App1	Sequence 305, App1
144	573	29.1	359	2	US-08-153-848-24	Sequence 24, App1	Sequence 549, App1
145	573	29.1	359	2	US-09-045-583-5	Sequence 5, App1	Sequence 1, App1
146	573	29.4	378	2	US-09-534-185-5	Sequence 5, App1	Sequence 1, App1
147	573	29.4	378	2	US-09-170-496D-24	Sequence 204, App1	Sequence 2, App1
148	570	28.9	378	2	US-09-088-383-750-2	Sequence 66, App1	Sequence 2, App1
149	570	28.9	378	1	US-08-383-751A-2	Sequence 66, App1	Sequence 2, App1
150	570	28.9	378	2	US-08-352-678-24	Sequence 2, App1	Sequence 2, App1
151	570	28.9	378	2	US-09-045-583-49	Sequence 24, App1	Sequence 2, App1
152	569	28.9	359	2	US-09-088-337B-24	Sequence 24, App1	Sequence 2, App1
153	570	28.9	359	4	PCT-US93-11153-24	Sequence 24, App1	Sequence 2, App1
154	570	28.9	378	2	US-09-929-583B-2	Sequence 2, App1	Sequence 2, App1
155	570	28.9	378	2	US-09-721-341-7	Sequence 7, App1	Sequence 2, App1
156	570	28.9	378	2	US-09-721-495B-7	Sequence 7, App1	Sequence 2, App1
157	570	28.9	378	4	PCT-US93-09636-2	Sequence 2, App1	Sequence 2, App1
158	569	28.9	357	2	US-09-266-464-2	Sequence 6, App1	Sequence 2, App1
159	569	28.9	357	2	US-09-170-496D-24	Sequence 1123, A	Sequence 7, App1
160	569	28.9	357	2	US-09-929-583B-2	Sequence 2, App1	Sequence 7, App1
161	569	28.9	357	2	US-09-966-755-2	Sequence 2, App1	Sequence 7, App1
162	569	28.9	357	2	US-09-522-752-2	Sequence 2, App1	Sequence 7, App1
163	569	28.9	369	2	US-09-721-341-7	Sequence 6, App1	Sequence 7, App1
164	569	28.9	369	2	US-09-721-495B-6	Sequence 6, App1	Sequence 7, App1
165	569	28.9	371	2	US-09-949-016-11223	Sequence 1123, A	Sequence 9, App1
166	566	28.7	357	2	US-09-170-496D-176	Sequence 176, App1	Sequence 4, App1
167	566	28.7	369	2	US-09-826-509-481	Sequence 481, App1	Sequence 4, App1
168	554	28.1	374	2	US-09-045-583-48	Sequence 48, App1	Sequence 168, App1
169	554	28.1	374	2	US-09-534-185-48	Sequence 48, App1	Sequence 509, App1
170	552	28.0	374	2	US-09-721-341-8	Sequence 8, App1	Sequence 38, App1
171	552	28.0	374	2	US-09-721-495B-8	Sequence 8, App1	Sequence 38, App1
172	541	27.5	355	1	US-07-759-568-1	Sequence 1, App1	Sequence 18, App1
173	541.5	27.5	355	1	US-08-450-393A-8	Sequence 8, App1	Sequence 8, App1

I protein - protein search, using SW model						
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Bioacceleration Ltd.						
On: March 29, 2006, 13:38:29 ; Search time 233 Seconds (without alignments)						
1132.479 Million cell updates/sec						
title: US-10-791-592-2	subject: 2166443 seqs, 705528306 residues	start-processing: 1970-01-01 00:00:00	last-processing: 2008-01-01 00:00:00	Maximum Match 99.9999% } Maximum Match 99.9999% } Listing first 1045 summaries	chosen parameters: 2166442	
scoring table: BLOSUM62	Gapop 10.0 , Gapext 0.5					
database : UniProt_05_80.*	1: uniprot_sprot: 2: uniprot_trembl: *:	1: uniprot_sprot: 2: uniprot_trembl: *:				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
result No.	Score	Query	Match	Length	DB	ID
1	1651.5	Q4VBL2 HUMAN	83.8	360	2	Q4VBL2
2	1614.5	CCR2_MACMU	82.0	360	1	CCR2_MACMU
3	1346.5	O51932 RAT	68.4	373	1	CCR2_MOUSE
4	1332.5	O51932 RAT	67.6	373	1	CCR2_MOUSE
5	1332.5	O51932 RAT	67.6	373	2	MOUSE
6	1227.5	O51932 CALMO	67.4	373	2	PIG
7	1252.5	O68628 RAT	63.3	354	2	Q68628
8	1247.5	O51932 CALMO	63.1	339	2	Q51932
9	1244.5	O51932 CALMO	63.1	339	2	Q51932
10	1244.5	O51932 CALMO	63.1	339	2	Q51932
11	1244.5	O51932 CALMO	63.1	352	2	Q51932
12	1244.5	O51932 CALMO	63.1	352	2	Q51932
13	1244.5	O51932 CALMO	63.1	354	1	CCR5_MOUSE
14	1243.5	O51932 CALMO	63.1	339	2	Q51932
15	1243.5	O51932 CALMO	63.1	352	2	Q51932
16	1241.5	O51932 CALMO	63.0	352	2	Q51932
17	1241.5	O51932 CALMO	63.0	352	2	Q51932
18	1241.5	O51932 CALMO	63.1	352	2	Q51932
19	1240.5	O51932 CALMO	62.9	339	2	Q51932
20	1239.5	O51932 CALMO	62.9	352	2	Q51932
21	1239.5	O51932 CALMO	62.9	352	2	Q51932
22	1238.5	O51932 CALMO	62.9	339	2	Q51932
23	1238.5	O51932 CALMO	62.8	339	2	Q51932
24	1238.5	O51932 CALMO	62.8	339	2	Q51932
25	1233.5	O51932 CALMO	62.7	339	2	Q51932
26	1233.5	O51932 CALMO	62.7	352	1	CCP10_CERPO
27	1233.5	O51932 CALMO	62.7	352	1	CCP10_HYLO
28	1233.5	O51932 CALMO	62.7	352	2	Q51932
29	1233.5	O51932 CALMO	62.7	352	2	Q51932
30	1233.5	O51932 CALMO	62.7	352	2	Q51932
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56	1230.5	O51932 CALMO	62.4	339	2	Q51932
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69	1230.5	O51932 CALMO	62.4	352	2	Q51932
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74	1230.5	O51932 CALMO	62.4	354	1	CCP10_CERPO
75	1229.5	O51932 CALMO	62.4	339	2	Q51932
76	1228.5	O51932 CALMO	62.3	339	2	Q51932
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81	1228.5	O51932 CALMO	62.3	339	2	Q51932
82	1228.5	O51932 CALMO	62.3	339	2	Q51932
83	1228.5	O51932 CALMO	62.3	339	2	Q51932
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87	1228.5	O51932 CALMO	62.3	352	1	CCP10_CERPO
88	1228.5	O51932 CALMO	62.3	352	1	CCP10_CERPO
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105	62.2	352	2	Q9XS99_9PRIM	Gorilla gor	Q9x99 homo sapien	Q9tvr0 cercopithec	Q9TUR0_CERMO	2	339
106	62.1	339	2	Q9UB79_HUMAN	Q9ub79 homo sapien	Q9un23 homo sapien	Q9tvr4 mandrillus	Q9TUR4_MANDRILLUS	2	339
107	62.1	339	2	Q9UN23_HUMAN	Q9un23 homo sapien	Q9un23 homo sapien	Q9tvr4 cercopithec	Q9TUR4_CERDI	2	339
108	62.1	339	2	Q9UN28_HUMAN	Q9un28 homo sapien	Q9un28 homo sapien	Q9tvr4 cercopithec	Q9TUR4_CERNE	2	352
109	62.1	339	2	Q9TQ70_PAPTA	Q9tq70 papio papio	Q9tq70 papio papio	Q9tvr4 cercopithec	Q9TUR4_CERNE	2	352
110	62.1	339	2	Q9TUR1_CERMO	Q9tvr1 cercopithec	Q9tvr1 cercopithec	Q9tvr4 cercopithec	Q9TUR4_CERMO	2	339
111	62.1	339	2	Q9TUR9_9PRIM	Q9tvr9 saguinus sp	Q9tvr9 saguinus sp	Q9tvr4 cercopithec	Q9TUR4_CERMO	2	339
112	62.1	339	2	Q9TUR9_HUMAN	Q9tvr9 homo sapien	Q9tvr9 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	339
113	62.1	339	2	Q9TUT1_PAPTA	Q9tut1 papio papio	Q9tut1 papio papio	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	339
114	62.1	339	2	Q9TUV1_AOTTR	Q9tuv1 aotus trivi	Q9tuv1 aotus trivi	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	339
115	62.1	339	2	Q9TUV5_PANTR	Q9tuv5 pan troglod	Q9tuv5 pan troglod	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	339
116	62.1	352	1	CCR5_HUMAN	P51681 homo sapien	P51681 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
117	62.1	352	1	CCR5_PYGNE	Q9tuv3 pygatrix n	Q9tuv3 pygatrix n	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
118	62.1	352	2	Q9ERK9_HUMAN	Q9erk9 homo sapien	Q9erk9 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
119	62.1	352	2	Q5Q1P1_HUMAN	Q5q1p1 homo sapien	Q5q1p1 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
120	62.1	352	2	Q95NC1_TheGE	Q95nc1 theropithec	Q95nc1 theropithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
121	62.1	352	2	Q95NC3_MITOCA	Q95nc3 miopithecus	Q95nc3 miopithecus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
122	62.1	352	2	Q9XTL14_COGLU	Q9xtl14 colobus guie	Q9xtl14 colobus guie	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
123	62.1	339	2	Q9TUR3_ERMPA	Q9tuv3 erythrocebus	Q9tuv3 erythrocebus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
124	62.1	339	2	Q9TUT4_MACME	Q9tut4 macaca nemae	Q9tut4 macaca nemae	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
125	62.1	339	2	Q9TUT10_MACMU	Q9tut10 macacus mili	Q9tut10 macacus mili	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
126	62.1	339	2	Q9TUT13_MACMU	Q9tut13 macaca mili	Q9tut13 macaca mili	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
127	62.1	339	2	Q9TUT8_CERDI	Q9tut8 cercopithec	Q9tut8 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
128	62.1	339	2	Q9TUV4_PANTR	Q9tuv4 pan troglod	Q9tuv4 pan troglod	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
129	62.1	339	2	Q9TUX1_HYLICO	Q9tux1 hylobates c	Q9tux1 hylobates c	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
130	62.1	340	2	Q9TUT2_MACMU	Q9tut2 macaca mili	Q9tut2 macaca mili	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
131	62.1	352	1	CCR5_PYGBL	Q9tuv80 pygatrix b	Q9tuv80 pygatrix b	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
132	62.1	352	1	CCR5_SEMEN	P61757 semnopithec	P61757 semnopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
133	62.1	352	1	CCR5_TRAFR	Q9tuv78 trachypithec	Q9tuv78 trachypithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
134	62.1	352	1	CCR5_TRAFH	Q9tuv79 trachypithec	Q9tuv79 trachypithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
135	62.1	352	2	Q97952_PYGAV	Q9tuv96 pygatrix a	Q9tuv96 pygatrix a	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
136	62.1	352	2	Q71726_TRAZCR	Q9tuv26 trachypithec	Q9tuv26 trachypithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
137	62.1	352	2	Q7J184_CBRPR	Q7tuv184 cercopithec	Q7tuv184 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
138	62.1	352	2	Q7JU34_PYRCRO	Q7tuv34 pygatrix r	Q7tuv34 pygatrix r	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
139	62.1	352	2	Q9TV50_PANTR	Q9tuv50 pan troglod	Q9tuv50 pan troglod	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
140	62.1	352	2	Q9XS35_MACNE	Q9xs35 macaca nemae	Q9xs35 macaca nemae	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
141	62.1	352	2	Q9XT76_9PRIM	Q9xt76 cercopithec	Q9xt76 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
142	62.0	339	2	Q9TUV8_GORGO	Q9tuv8 gorilla gor	Q9tuv8 gorilla gor	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
143	62.0	352	2	Q9M221_LAQLA	Q9m221 lagotrix l	Q9m221 lagotrix l	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
144	62.0	339	2	Q9UB77_HUMAN	Q9ub77 homo sapien	Q9ub77 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
145	62.0	339	2	Q9UN77_HUMAN	Q9un77 homo sapien	Q9un77 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
146	62.0	339	2	Q9TUV8_PAPTA	Q9tuv8 papio papio	Q9tuv8 papio papio	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
147	62.0	339	2	Q9TUT5_MACNE	Q9tut5 macaca nemae	Q9tut5 macaca nemae	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
148	62.0	339	2	Q9TUV8_GORGO	Q9tuv8 gorilla gorilla	Q9tuv8 gorilla gorilla	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
149	62.0	352	2	Q9M222_NASLIA	Q9m222 nasalis lar	Q9m222 nasalis lar	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
150	62.0	352	2	Q9TUV44_ERMPA	Q9tuv44 erythrocebus	Q9tuv44 erythrocebus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
151	62.0	352	2	Q9XTL3_PAPTA	Q9xtl3 papio anubis	Q9xtl3 papio anubis	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
152	62.0	339	2	Q9UN24_HUMAN	Q9un24 homo sapien	Q9un24 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
153	62.0	339	2	Q9TUV4_CERAE	Q9tuv4 cercopithec	Q9tuv4 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
154	62.0	339	2	Q9TUV6_9PRIM	Q9tuv6 macaca fasciata	Q9tuv6 macaca fasciata	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
155	62.0	352	2	Q9TEN22_MACFA	Q9ten22 macaca fasciata	Q9ten22 macaca fasciata	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
156	62.0	339	2	Q9TUR9_CERMO	Q9tuv9 cercopithec	Q9tuv9 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
157	62.0	339	2	Q9TUR2_ERMPA	Q9tuv2 erythrocebus	Q9tuv2 erythrocebus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
158	62.0	339	2	Q9TUT16_MACNE	Q9tut16 macaca nemae	Q9tut16 macaca nemae	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
159	62.0	339	2	Q9TUV4_HUMAN	Q9tuv4 cercopithec	Q9tuv4 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
160	62.0	339	2	CCR5_CERPY	Q9tuv59 cercopithec	Q9tuv59 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
161	62.0	339	2	Q9TUV8_9PRIM	Q9tuv8 cercopithec	Q9tuv8 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
162	62.0	339	2	Q9TUV13_PAPTA	Q9tuv13 papio anubis	Q9tuv13 papio anubis	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
163	62.0	339	2	Q9TUV6_ALPCA	Q9tuv6 alouatta caraya	Q9tuv6 alouatta caraya	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
164	62.0	339	2	Q9TUV4_HUMAN	Q9tuv4 cercopithec	Q9tuv4 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
165	62.0	339	2	Q9TUV7_PAPTA	Q9tuv7 papio papio	Q9tuv7 papio papio	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
166	62.0	339	2	Q9QIN9_HUMAN	Q9qin9 homo sapien	Q9qin9 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
167	62.0	339	2	CCR5_CERPY	Q9tuv8 cercopithec	Q9tuv8 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
168	62.0	339	2	Q9TUV44_9PRIM	Q9tuv44 cercopithec	Q9tuv44 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
169	62.0	339	2	Q9TUV6_CERAE	Q9tuv6 cercopithec	Q9tuv6 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
170	62.0	339	2	Q9TUV16_MACNE	Q9tuv16 macaca nemae	Q9tuv16 macaca nemae	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
171	62.0	339	2	Q9TUV7_PAPTA	Q9tuv7 cercopithec	Q9tuv7 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
172	62.0	339	2	Q9QIN9_HUMAN	Q9qin9 homo sapien	Q9qin9 homo sapien	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
173	62.0	339	2	Q9TUV11_PANTR	Q9tuv11 pan troglod	Q9tuv11 pan troglod	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
174	62.0	339	2	Q95NC6_TRAJO	Q95nc6 trachypithecus	Q95nc6 trachypithecus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
175	62.0	339	2	Q9TUV4_CERAE	Q9tuv4 cercopithec	Q9tuv4 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
176	62.0	339	2	Q9TUV4_HUMAN	Q9tuv4 erythrocebus	Q9tuv4 erythrocebus	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
177	62.0	339	2	Q9TUV8_9PRIM	Q9tuv8 cercopithec	Q9tuv8 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352

178	62.0	339	2	Q9TUV12_HUMAN	Q9tuv12 cercopithec	Q9tuv12 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
179	62.0	339	2	Q9TUV13_HUMAN	Q9tuv13 cercopithec	Q9tuv13 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
180	62.0	339	2	Q9TUV14_HUMAN	Q9tuv14 cercopithec	Q9tuv14 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
181	62.0	339	2	Q9TUV15_HUMAN	Q9tuv15 cercopithec	Q9tuv15 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
182	62.0	339	2	Q9TUV16_HUMAN	Q9tuv16 cercopithec	Q9tuv16 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
183	62.0	339	2	Q9TUV17_HUMAN	Q9tuv17 cercopithec	Q9tuv17 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
184	62.0	339	2	Q9TUV18_HUMAN	Q9tuv18 cercopithec	Q9tuv18 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
185	62.0	339	2	Q9TUV19_HUMAN	Q9tuv19 cercopithec	Q9tuv19 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
186	62.0	339	2	Q9TUV20_HUMAN	Q9tuv20 cercopithec	Q9tuv20 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
187	62.0	339	2	Q9TUV21_HUMAN	Q9tuv21 cercopithec	Q9tuv21 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
188	62.0	339	2	Q9TUV22_HUMAN	Q9tuv22 cercopithec	Q9tuv22 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
189	62.0	339	2	Q9TUV23_HUMAN	Q9tuv23 cercopithec	Q9tuv23 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
190	62.0	339	2	Q9TUV24_HUMAN	Q9tuv24 cercopithec	Q9tuv24 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
191	62.0	339	2	Q9TUV25_HUMAN	Q9tuv25 cercopithec	Q9tuv25 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
192	62.0	339	2	Q9TUV26_HUMAN	Q9tuv26 cercopithec	Q9tuv26 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
193	62.0	339	2	Q9TUV27_HUMAN	Q9tuv27 cercopithec	Q9tuv27 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
194	62.0	339	2	Q9TUV28_HUMAN	Q9tuv28 cercopithec	Q9tuv28 cercopithec	Q9tvr4 cercopithec	Q9TUR4_HUMAN	2	352
195	62.0	339	2	Q9TUV29_HUMAN	Q9tuv29 cercopithec	Q9tuv29 cercopithec	Q9tvr4			

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OM protein - protein search, using sw mode1

Run on: March 29, 2006, 14:01:34 ; Search time 232 Seconds

(without alignment(s), 1137.360 Million cell updates/sec)

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTRSRFLRNTNNSGEVV.....GKGRSIGRAPEASLQDKEGA 374

Scoring table: Oligo Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 10

Total number of hits satisfying chosen parameters: 298

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 90 summaries

Database : UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	374	100.0	374	1	CCR2_HUMAN	Q4VBL2_HUMAN	P41597 homo sapien
2	313	83.7	360	2	Q4VBL2_HUMAN	Q4VBL2_homo sapien	
3	105	28.1	105	2	Q6Y3M6_PANTR	Q6Y3M6_pan troglod	
4	105	28.1	105	2	Q6Y3M6_PANTR	Q6Y3M6_gorilla gorilla gorilla	
5	100	26.7	105	2	Q6Y3M7_PANTR	Q6Y3M7_pan troglod	
6	93	24.9	140	2	Q95950_HUMAN	Q95950_homo sapien	
7	88	23.5	105	2	Q6Y3M9_PONPY	Q6Y3M9_pongo pygmaeus	
8	59	15.8	105	2	Q6Y3M3_MACMU	Q6Y3M3_macaca mula	
9	59	15.8	105	2	Q6Y3M5_PAPHA	Q6Y3M5_papio hamadryas	
10	59	15.8	105	2	Q6Y3N0_MACMU	Q6Y3N0_macaca fasciata	
11	59	15.8	360	2	CCR2_MACMU	Q18793_macaca mula	
12	51	13.6	86	2	Q6Y3N5_CALJA	Q6Y3N5_callithrix jacchus	
13	49	13.1	105	2	Q6Y3N1_HYLIA	Q6Y3N1_hylobates lar	
14	47	12.6	373	2	CCR2_RAT	Q55193_rattus norvegicus	
15	46	12.3	316	2	Q9TUV7_9PRIM	Q9TUV7_saginus sp	
16	46	12.3	339	2	Q9TUV5_9PRIM	Q9TUV5_saginus sp	
17	46	12.3	339	2	Q9TUV6_9PRIM	Q9TUV6_saginus sp	
18	46	12.3	339	2	Q9TUV8_9PRIM	Q9TUV8_saginus sp	
19	46	12.3	339	2	Q9TUV9_9PRIM	Q9TUV9_saginus sp	
20	46	12.3	339	2	Q9TUV0_9PRIM	Q9TUV0_saginus sp	
21	46	12.3	339	2	Q9TUV1_9PRIM	Q9TUV1_saginus sp	
22	46	12.3	373	2	Q6Y3V2_PIG	Q6Y3V2_sus scrofa	
23	43	11.5	339	2	Q9TUV2_9PRIM	Q9TUV2_saginus sp	
24	43	11.5	373	1	CCR2_MOUSE	P51683_mus musculus	
25	43	11.5	373	2	Q54358_MOOS	P51398_mus musculus	
26	39	10.4	334	2	Q9TUQ7_BRPA	Q9TUQ7_erythrocебу	
27	39	10.4	339	2	Q9TQ22_GORGO	Q9TQ22_gorilla gorilla gorilla	
28	39	10.4	339	2	Q9TQ01_MACPA	Q9TQ01_macaca fasciata	
29	39	10.4	339	2	Q9TQ01_MACMU	Q9TQ01_macaca mula	
30	39	10.4	339	2	Q9TQ02_MACMU	Q9TQ02_macaca nemestrina	
31	39	10.4	339	2	Q9TQ03_CALJA	Q9TQ03_callithrix jacchus	

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	374	100.0	374	1	CCR2_HUMAN	P41597 homo sapien	
2	313	83.7	360	2	Q4VBL2_HUMAN	Q4VBL2_homo sapien	
3	105	28.1	105	2	Q6Y3M6_PANTR	Q6Y3M6_pan troglod	
4	105	28.1	105	2	Q6Y3M6_PANTR	Q6Y3M6_gorilla gorilla gorilla	
5	100	26.7	105	2	Q6Y3M7_PANTR	Q6Y3M7_pan troglod	
6	93	24.9	140	2	Q95950_HUMAN	Q95950_homo sapien	
7	88	23.5	105	2	Q6Y3M9_PONPY	Q6Y3M9_pongo pygmaeus	
8	59	15.8	105	2	Q6Y3M3_MACMU	Q6Y3M3_macaca mula	
9	59	15.8	105	2	Q6Y3M5_PAPHA	Q6Y3M5_papio hamadryas	
10	59	15.8	105	2	Q6Y3N0_MACMU	Q6Y3N0_macaca fasciata	
11	59	15.8	360	2	CCR2_MACMU	Q18793_macaca mula	
12	51	13.6	86	2	Q6Y3N5_CALJA	Q6Y3N5_callithrix jacchus	
13	49	13.1	105	2	Q6Y3N1_HYLIA	Q6Y3N1_hylobates lar	
14	47	12.6	373	2	CCR2_RAT	Q55193_rattus norvegicus	
15	46	12.3	316	2	Q9TUV7_9PRIM	Q9TUV7_saginus sp	
16	46	12.3	339	2	Q9TUV5_9PRIM	Q9TUV5_saginus sp	
17	46	12.3	339	2	Q9TUV6_9PRIM	Q9TUV6_saginus sp	
18	46	12.3	339	2	Q9TUV8_9PRIM	Q9TUV8_saginus sp	
19	46	12.3	339	2	Q9TUV9_9PRIM	Q9TUV9_saginus sp	
20	46	12.3	339	2	Q9TUV0_9PRIM	Q9TUV0_saginus sp	
21	46	12.3	339	2	Q9TUV1_9PRIM	Q9TUV1_saginus sp	
22	46	12.3	373	2	Q6Y3V2_PIG	Q6Y3V2_sus scrofa	
23	43	11.5	339	2	Q9TUV2_9PRIM	Q9TUV2_saginus sp	
24	43	11.5	373	1	CCR2_MOUSE	P51683_mus musculus	
25	43	11.5	373	2	Q54358_MOOS	P51398_mus musculus	
26	39	10.4	334	2	Q9TUQ7_BRPA	Q9TUQ7_erythrocебу	
27	39	10.4	339	2	Q9TQ22_GORGO	Q9TQ22_gorilla gorilla gorilla	
28	39	10.4	339	2	Q9TQ01_MACPA	Q9TQ01_macaca fasciata	
29	39	10.4	339	2	Q9TQ01_MACMU	Q9TQ01_macaca mula	
30	39	10.4	339	2	Q9TQ02_MACMU	Q9TQ02_macaca nemestrina	
31	39	10.4	339	2	Q9TQ03_CALJA	Q9TQ03_callithrix jacchus	

ALIGNMENTS

RESULT 1	CCR2_HUMAN	STANDARD	PRT;	374 AA.
ID	AC P41597;			
	DT 01-NOV-1995 (Rel. 32, Created)			
	DT 01-MAY-2005 (Rel. 32, Last sequence update)			
	DT 10-MAY-2005 (Rel. 47, Last annotation update)			
	DE C-C Chemokine receptor type 2 (C-C CR-2) (CCR-2)			
	DB (Monocyte chemoattractant protein 1 receptor) (MCP-1-R)			
	DB 062743 cercocebus			

GN	Name=CCR2; Synonyms=CMKBR2;	RA	Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
OS	Homo sapiens (Human);	RA	Chakravarty L., Kolattukudy P.E.,
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RT	"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	RT	has tyrosine sulfation in a conserved extracellular N-terminal
NCBI_TAXID	9606;	RT	region.";
RN	[1]	RL	J. Immunol. 165:52295-5303 (2000).
RX	NUCLEOTIDE SEQUENCE.	CC	- - FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
RX	MEDLINE=94195621; PubMed=8146186;	CC	- - Transduces a signal by increasing the intracellular calcium ions
RA	Charo I.P., Myers S.J., Herman A., Franci C., Connolly A.J.,	CC	level. Alternative coreceptor with CD4 for HIV-1 infection.
RA	Coughlin S.R.,	CC	- - SUBCELLULAR LOCATION: Integral membrane protein.
RT	"Molecular cloning and functional expression of two monocyte	CC	- - ALTERNATIVE PRODUCTS:
RT	chemoattractant protein 1 receptors reveals alternative splicing of	CC	Event=Alternative splicing; Named isoforms=2;
RT	the carboxyl-terminal tails";	CC	Name=A;
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).	CC	Isoid=P41597-1; Sequence=Displayed;
RN	[2]	CC	Name=B;
RX	NUCLEOTIDE SEQUENCE.	CC	Isoid=P41597-2; Sequence=vSP_001893;
RP	MEDLINE=94324942; PubMed=8048929;	CC	- - PTM: N-Glycosylation. Belongs to the G-protein coupled receptor 1 family.
RX	Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;	CC	- - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
RA	"cDNA cloning and functional expression of a human monocyte	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
RT	chemoattractant protein 1 receptor.";	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RT	'RL Biochem. Biophys. Res. Commun. 202:1156-1162 (1994).	CC	the European Bioinformatics Institute. There are no restrictions on its
RN	[3]	CC	use as long as its content is in no way modified and this statement is not
RN	removed.	CC	removed.
RX	NUCLEOTIDE SEQUENCE.	CC	EMBL: U03882; AA11919.1; -; mRNA.
RP	MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;	DR	EMBL: U03905; AA119120.1; -; mRNA.
RT	"Organization and differential expression of the human monocyte	DR	EMBL: D29984; BAA06253.1; -; mRNA.
RT	chemoattractant protein 1 receptor gene. Evidence for the role of the	DR	EMBL: U080924; AAC51637.1; -; Genomic DNA.
RT	carboxyl-terminal tail in receptor trafficking.";	DR	EMBL: U080924; AAC51636.1; -; Genomic DNA.
RL	J. Biol. Chem. 272:1038-1045 (1997).	DR	EMBL: U95626; AAC57791.1; -; Genomic DNA.
RN	[4]	DR	EMBL: U95626; AAC57792.1; -; Genomic DNA.
RX	NUCLEOTIDE SEQUENCE.	DR	EMBL: AF45440; AA11600.1; -; Genomic DNA.
RP	McCombie W.R., Wilson R., Chen B., Gibbs R., Zuo L., Johnson D.,	DR	EMBL: BC074751; AAH74751.1; -; mRNA.
RA	Nhan M., Parnell L., Dediha N., Ansari A., Mardis E., Schutz K.,	DR	PIR: I38450; I38450.
RA	Gnoj L., La Bastide P., Gresco T., Touchman J., Muzny D.,	DR	PIR: JC2443; JC2443.
RA	Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,	DR	PDB: 1KAD; Model: A=1-313.
RA	Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,	DR	PDB: 1KF1; Model: A=1-313.
RA	Sacripanti J.L., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,	DR	HGNC: HGNC:1603; CCR2.
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJU databases.	DR	MIM: 601267; -
RN	[5]	DR	GO: 00105887; C:integral to plasma membrane; TAS.
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ILE-64 AND GLU-355.	DR	GO: 00105886; C:plasma membrane; TAS.
RA	Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,	DR	GO: 0005625; C:soluble fraction; TAS.
RA	Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;	DR	GO: 0004555; P:chemokine receptor activity; TAS.
RA	"SeattleSNPs. NHLBI HL66822 program for genomic applications, UW-	DR	GO: 0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.
RT	FHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";	DR	GO: 0006368; P:cellular defense response; TAS.
RN	Submitted (SEP-2002) to the EMBL/GenBank/DBJU databases.	DR	GO: 0006935; P:chemotaxis; TAS.
[6]	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).	DR	GO: 00100694; P:inflammatory response; TAS.
RP	MEDLINE=22388357; PubMed=12477932; DOI=10.1073/pnas.242603899;	DR	GO: 0007204; P:negative regulation of cytosolic calcium io. . .; TAS.
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	DR	GO: 00100588; P:negative regulation of cytosolic calcium io. . .; TAS.
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	DR	InterPro: IPR002337; CC:2 receptor.
RA	Altchuler S.F., Zeeberg B., Buetow K.E., Schaefer C.F., Bhat N.K.,	DR	InterPro: IPR003555; ChkM1ne receptor.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsileh F.,	DR	InterPro: IPR000276; GPCR_Rhodopsin.
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	DR	Pfam: PF000001; 7em 1; 1.
RA	Stapleton M., Soares M.B., McDonald M.P., Casavant T.L., Scheetz T.B.,	DR	PRINTS: PR00657; CCHEMOKINER.
RA	Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,	DR	PRINTS: PR001077; CHEMOKINER2.
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	DR	PROSITE: PS00237; G-PROTEIN RECEP_F1_1; 1.
RA	Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	DR	PROSITE: PS00237; G-PROTEIN RECEP_F1_2; 1.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	DR	3D-structure: Alternative splicing; G-protein coupled receptor;
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	KW	Glycoprotein; Polymorphism; Receptor; Sulfation; Transducer;
RA	Fahney J., Heitton E., Kettmann M., Madden A., Rodrigues S., Sanchez A.,	KW	Transmembrane.
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	FT	TOPO DOM 1 42 Extracellular (Potential).
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	FT	TRANSMEM 43 70 Cytoplasmic (Potential).
RA	Rodriguez A.C., Grimes J.W., Schmitz J., Myers R.M.,	FT	TOPO DOM 71 80 Cytoplasmic (Potential).
RA	Butterfield Y.S.N., Krywawych M.I., Skalska U., Smialius D.E.,	FT	TRANSMEM 81 100 Extracellular (Potential).
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;	FT	TOPO DOM 101 114 Extracellular (Potential).
RT	"Generation and initial analysis of more than 15,000 full-length human	FT	TRANSMEM 115 136 3 (Potential).
RT	and mouse cDNA sequences.";	FT	TRANSMEM 137 153 Cytoplasmic (Potential).
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	FT	TRANSMEM 154 178 Extracellular (Potential).
RN	[7]	FT	TOPO DOM 179 206 5 (Potential).
RP	SULFATION OF TYR-26, AND N-GLYCOSYLATION.	FT	TRANSMEM 207 226
RX	MEDLINE=20501139; PubMed=11046064;		

GenCore version 5.1.7
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OM protein - protein search, using sw model 1

Run on: March 29, 2006, 14:04:54 ; Search time 41 Seconds

(without alignments)

877.685 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTRSRFTNTNSGEEV..... GKGRSIGRAPEASLQDKEGA 374

Scoring table: OLTGO Gapop 60.0 , Gapext 60.0
Searched: 283416 seqs, 96216763 residues

Word size : 10
Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 90 summaries

Database : PIR 80.0;
1: pir1:/*
2: pir2:/*
3: pir3:/*
4: pir4:/*

Total number of hits satisfying chosen parameters: 19

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	374	100.0	374	2	I38450		chemokine (C-C) receptor 1
2	313	83.7	360	2	A43113		chemokine (C-C) receptor 1
3	26	7.0	352	2	G02416		chemokine (C-C) receptor 1
4	22	5.9	355	2	A51177		chemokine (C-C) receptor 1
5	22	5.9	355	2	I49339		macrophage inflammatory protein 1 alpha receptor
6	22	5.9	355	2	I49341		chemokine (C-C) receptor 1
7	22	5.9	360	2	JC1610		chemokine (C-C) receptor 1
8	12	3.2	360	2	JC4587		chemokine (C-C) receptor 1
9	12	3.2	383	2	S63666		chemokine (C-C) receptor 1
10	12	3.2	383	2	S55594		chemokine (C-C) receptor 1
11	11	2.9	341	2	S13636		chemokine (C-C) receptor 1
12	11	2.9	342	2	S13638		chemokine (C-C) receptor 1
13	11	2.9	354	2	I58186		chemokine (C-C) receptor 1
14	10	2.7	308	2	I50241		chemokine (C-C) receptor 1
15	10	2.7	327	2	S56162		chemokine (C-C) receptor 1
16	10	2.7	333	2	S78136		chemokine (C-C) receptor 1
17	10	2.7	372	2	S26667		chemokine (C-C) receptor 1
18	10	2.7	374	2	S42628		chemokine (C-C) receptor 1
19	10	2.7	374	2	S322785		chemokine (C-C) receptor 1

ALIGNMENTS

RESULT 1
JC2443 chemokine (C-C) receptor 2, splice form B - human
N: Alternate names: C-C CCR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 2, splice form B - human
C: Species: Homo sapiens (man)
C: Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C: Accession: JC2443 ; 138463
R. Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A: Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 2, splice form B - human
A: Reference number: JC2443 ; MUID:94324942; PMID:8048929
A: Accession: JC2443
A: Molecule type: mRNA

A; Residues: 1-360 <YAM>
 A; Cross-references: UNIPROT:PA1557; UNIPARC:UPI000002A69C; DDBJ: D29984; NID: 9531246; PID: R; Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A; Title: Molecular cloning and functional expression of two monocyte chemoattractant protein-1 genes.
 A; Reference number: A53477; MUID: 94195821; PMID: 8146786
 A; Accession: I38463
 A; Status: Preliminary
 A; Molecule type: mRNA
 A; Residues: 1-360 <RES>
 A; Cross-references: UNIPARC:UPI00002A69C; EMBL:U03905; NID:9472557; PIDN:AAA19120-1; PI
 C; Genetics:
 A; Gene: GDB: CMKBR2
 A; MAF position: 3021-3021
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
 F; 13-70/Domain: transmembrane #status predicted <TM1>
 F; 81-100/Domain: transmembrane #status predicted <TM2>
 F; 154-178/Domain: transmembrane #status predicted <TM3>
 *F; 207-226/Domain: transmembrane #status predicted <TM4>
 F; 244-268/Domain: transmembrane #status predicted <TM5>
 F; 287-309/Domain: transmembrane #status predicted <TM7>
 F; 14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 13-198/Disulfide bonds: #status predicted

Query Match 83.7%; Score 313; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 5e-30+; Mismatches 0; Indels 0; Gaps 0;
 Matches 313; Conservative 0; Mismatches 0;

Qy 1 MLPSRSRFLRTNTESGEVTTFDYDVGAPCKPDKVQIGAQLLPPLVSLVPIFGFTGN 60
 Db 1 MLPSRSRFLRTNTESGEVTTFDYDVGAPCKPDKVQIGAQLLPPLVSLVPIFGFTGN 60
 Qy 61 MLVYLILINCKKIKLTDYLLNIAISDILFLITPLWAHSAAANEWFGNAMCKLFTGTY 120
 Db 61 MLVYLILINCKKIKLTDYLLNIAISDILFLITPLWAHSAAANEWFGNAMCKLFTGTY 120
 Qy 121 HIGHFGGIIPIIILITDYLAIHVAFALKARTTFGVTISVITWLVAFASVPGIIFTK 180
 Db 121 HIGHFGGIIPIIILITDYLAIHVAFALKARTTFGVTISVITWLVAFASVPGIIFTK 180
 Qy 181 CQEDSVTVCGPYPRGMNPFHTMRNINLVLPLIMIVCSGILKTLRCLNEKRR 240
 Db 181 CQEDSVTVCGPYPRGMNPFHTMRNINLVLPLIMIVCSGILKTLRCLNEKRR 240
 Qy 241 AYRIFTMIMIVYFLWTPNIVLINTFOBFFGLSNCESTSQLDQATOVTETLGMTKCI 300
 Db 241 AYRIFTMIMIVYFLWTPNIVLINTFOBFFGLSNCESTSQLDQATOVTETLGMTKCI 300
 Qy 301 NPIIYAFVGSEKFR 313
 Db 301 NPIIYAFVGSEKFR 313

RESULT 3
 A43113
 chemokine (C-C) receptor 5 - human
 N; Alternative names: C-C CKR-5; CCRT5
 C; Species: Homo sapiens (man)
 C; Accession: A43113; S71808; A58334; A58833; G02653; A58333
 C; Accession: A43113; S71808; A58334; A58833; G02653; A58333
 A; Reference number: A43113; MUID: 96241590; PMID: 8633485
 A; Accession: A43113
 A; Molecule type: mRNA
 A; Residues: 1-352 <SAM1>
 A; Cross-references: UNIPARC:UPI000000D955; GB:X91492; NID: 91262810; PIDN: CAA62796_1; PI
 R; Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
 Biochemistry 35, 3362-3367, 1996
 A; Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
 A; Reference number: A43113; MUID: 96241590; PMID: 8633485

Nature 382, 722-725, 1996
 A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of A; Reference number: S71808; MUID: 96345670; PMID: 871444
 A; Accession: S71808
 A; Status: nucleic acid sequence not shown; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residue: 182-206; 207-230 <SAM2>
 A; Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA; <SAM3>
 A; Status: nucleic acid sequence not shown; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-184; IKDISHLGPAACGHILLGPNKNSASVK
 A; Cross-references: UNIPARC:UPI00001778E9; UNIPARC:UPI00001778EA
 A; Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to Yersinia plague infection
 R; Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
 J. Leukoc. Biol. 60, 147-152, 1996
 A; Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
 A; Reference number: A58832; MUID: 96295970; PMID: 8639919
 A; Accession: A58832
 A; Molecule type: mRNA
 A; Residues: 1-352 <COM1>
 A; Cross-references: UNIPARC:UPI000000D955; GB:U57840; NID: 9102408; PIDN: AAB17071_1; PID: R; Combadiere, C.
 A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
 R; Combadiere, C.
 Submitted to the EMBL Data Library, May 1996
 A; Reference number: H01541
 A; Accession: G02653
 A; Status: translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-89 /' 91-352 <COM2>
 A; Cross-references: UNIPARC:UPI00001778BB; EMBL:U57840
 R; Report: C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
 J. Biol. Chem. 271, 17161-17166, 1996
 A; Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
 A; Reference number: A58833; MUID: 96291862; PMID: 8663314
 A; Accession: A58833
 A; Molecule type: mRNA
 A; Residues: 1-352 <RAP>
 A; Cross-references: UNIPARC:UPI000000D955; GB:U54994; NID: 91457945; PIDN: AAC5098_1; PID: R; Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see C; Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C; Genetics:
 A; Gene: CMKBR5; CCR5; CKR5; CC-CKR-5; CKR5; ChemR13
 A; Cross-references: GDB:1240510; OMIM: 601373
 A; Map position: 3p21-3p21
 C; Function:
 A; Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
 A; Note: Probably acts to control granulocyte proliferation and differentiation
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
 F; 132-156/Domain: transmembrane #status predicted <TM1>
 F; 157-187/Domain: transmembrane #status predicted <TM2>
 F; 103-124/Domain: transmembrane #status predicted <TM3>
 F; 142-166/Domain: transmembrane #status predicted <TM4>
 F; 193-218/Domain: transmembrane #status predicted <TM5>
 F; 236-257/Domain: transmembrane #status predicted <TM6>
 F; 285-300/Domain: transmembrane #status predicted <TM7>
 F; 20-269,101-179/Disulfide bonds: #status predicted
 F; 268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F; 340,343/Binding site: phosphate (Thr) (covalent) #status predicted
 Query Match 7.0%; Score 26; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.8e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 218 MVICYSGLIKTLILRCRNEKGRHRAVR 243
 Db 210 MVICYSGLIKTLILRCRNEKGRHRAVR 235
 RESULT 4

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OM protein - protein search, using bw model

Run on: March 29, 2006, 14:01:15 ; Search time 190 Seconds

(without alignments)
864.882 Million cell. updates/sec

Title: US-10-791-592-2
Perfect score: 374
Sequence: 1 MLSTRSRPIRNTNSGEEV.....GKGRSIGRAPEASLQDGKA 374

Scoring table: Oligo
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 433378781 residues

Word size: 10

Total number of hits satisfying chosen parameters: 374

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp003s:*

7: geneseqp2003s:*

8: geneseqp2004s:*

9: geneseqp005s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	374	100.0	374	2	AAR79165		Aar79165 Human mon
2	374	100.0	374	4	AAG80107		Aag80107 Human CCR
3	374	100.0	374	6	ABU09083		Abu09083 Human che
4	374	100.0	374	7	ADD44861		Add44861 Human Pro
5	374	100.0	374	7	ADD44865		Add44865 Human Pro
6	374	100.0	374	7	ADP65146		Adp65146 Human che
7	374	100.0	374	8	ADO2221		Ado2221 Human GPC
8	374	100.0	374	8	ADQ67847		Adq67847 Human che
9	374	100.0	374	9	ADY15762		Ady15762 PRO polyp
10	374	100.0	374	9	ADY19514		Ady19514 PRO polyp
11	374	100.0	374	9	ADZ11713		Adz11713 Human che
12	374	100.0	374	9	ADZ75584		Adz75584 Human CCR
13	374	100.0	374	9	AEB22129		Aeb22129 Human che
14	374	100.0	374	9	AEB94404		Aeb94404 Human C-C
15	344	92.0	344	5	ABG2881		Abg2881 Class I r
16	344	92.0	344	6	ABU61655		Abu61655 Human mon
17	344	92.0	344	7	ADF72129		Adf72129 Human G-P
18	344	92.0	344	8	ADP85217		Adp85217 Human MCP
19	313	83.7	360	2	AAR79166		Aar79166 Human mon
20	313	83.7	360	2	AAW35533		Aaw35533 Human mon
21	313	83.7	360	4	AAG80108		Aag80108 Human CCR
22	313	83.7	360	4	AAU07614		Aau07614 Human w1
23	313	83.7	360	4	ABP97725		Abp97725 Amiino aci
24	313	83.7	360	6	ABP81987		Abp81987 Human C-C

RESULT 1
AAR79165

ALIGNMENTS

ID	AAR79165	standard; protein; 374 AA.	CC	field.)
XX	AC	AAR79165;	XX	Sequence 374 AA;
XX	DT	25-MAR-2003 (revised)	Query Match	100.0%;
DT	29-DEC-1995 (first entry)	Best Local Similarity	100.0%;	
XX	XX	Matches 374;	Pred. No. 0;	
DB	XX	Conservative 0;	Mismatches 0;	
XX	XX	Indels 0;	Gaps 0;	
KW	Human monocyte chemoattractant protein-1 receptor MCP-1RA.			
OS	Homo sapiens.			
XX	Key	Location/Qualifiers		
FT	Domain	1..48 /label= extracellular	Qy	1 MUSTSRSPIRINTNESGREVTIFFDYYGAPCHKFDFYKQIGAQLLPLPLSFLVIFGVGN 60
FT	Domain	49..70 /label= transmembrane	Db	1 MUSTSRSPIRINTNESGREVTIFFDYYGAPCHKFDFYKQIGAQLLPLPLSFLVIFGVGN 60
FT	Domain	80..700 /label= transmembrane	Qy	61 MLVVLILINCKKLCKLTDIYLILNLAISDLFLITLPIWAHSANEVFGNAMCKLFTGLY 120
FT	Domain	701..136 /label= transmembrane	Db	61 MLVVLILINCKKLCKLTDIYLILNLAISDLFLITLPIWAHSANEVFGNAMCKLFTGLY 120
FT	Domain	137..154 /label= transmembrane	Qy	121 HIGYFGGIPPFILLTIDYLAVHAPALKARTVTFGVTSVITWLVAFAVSPGIFTK 180
FT	Domain	155..178 /label= transmembrane	Db	121 HIGYFGGIPPFILLTIDYLAVHAPALKARTVTFGVTSVITWLVAFAVSPGIFTK 180
FT	Domain	204..231 /label= transmembrane	Qy	181 COKEDSYVCGPYFPRGMNNFTIMMRNLLGVLPLLIMVICYSGLILKTLRGRNECKGRHR 240
FT	Domain	244..268 /label= transmembrane	Db	181 COKEDSYVCGPYFPRGMNNFTIMMRNLLGVLPLLIMVICYSGLILKTLRGRNECKGRHR 240
FT	Domain	269..313 /label= transmembrane	Qy	241 AVRVIFTIMIVXFLWTPYNTVILNNTFQEPFGLSNCESTSISDQATQVTTETLGMTHCC1 300
FT	Domain	314..375 /label= carboxyl tail	Db	241 AVRVIFTIMIVXFLWTPYNTVILNNTFQEPFGLSNCESTSISDQATQVTTETLGMTHCC1 300
XX	PN	W09519436-A1.	Qy	301 NPIIYAFYGEKRSFLPHIALGCRIAPIQKPVCGGPYVRPGKVNKVTTQGLLDRGRGKGS1 360
XX	PD	20-JUL-1995.	Db	301 NPIIYAFYGEKRSFLPHIALGCRIAPIQKPVCGGPYVRPGKVNKVTTQGLLDRGRGKGS1 360
XX	PP	11-JAN-1995;	Qy	361 GRAPEASLQDKEGA 374
XX	PR	13-JAN-1994;	Db	361 GRAPEASLQDKEGA 374
XX	PA	94US-00182962.	RESULT 2	
(REGC)	UNIV CALIFORNIA.		ID	AAG80107 standard; protein; 374 AA.
XX	PI	Charo I., Coughlin S.,	XX	AAG80107;
XX	XX		DT	17-JAN-2002 (first entry)
DR	1995-263866/34.		XX	Human CCR2a protein.
NN-PSDB;	AAQ96297.		XX	Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytosaratic; antiinflammatory; antiallergic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
PS	WPI: 1995-263866/34.		XX	KW Homo sapiens.
XX	DR		OS	W0200172830-A2.
XX	NN		XX	04-OCT-2001.
XX	XX		XX	02-APR-2001; 2001WO-EP003708.
CC	XX	DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.	XX	31-MAR-2000; 2000DE-01016013.
CC	XX	for identifying antagonists and for treating diseases characterised by	XX	
CC	XX	monocytic infiltrates.	XX	
CC	XX	Claim 2: Fig 1; 8app; English.	XX	
CC	XX	To identify and clone new members of the chemokine receptor gene family, degenerate oligo primers were designed to correspond to the conserved sequences R79167 in the second and R79168 in the third transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the HUMSTRS orphan receptor (Genbank Accession #M99293. The degenerate oligo incorporating EcoRI and XbaI sites at their 5' ends are Q96299 and Q96300. Amplification of cDNA derived from MM6 cells with the primers yielded a number of PCR products. One cDNA appeared to encode a novel protein. To obtain a full-length version of this clone, a MM6 cDNA library was constructed in pFROG and probed with the PCR product. A 2.1 kb cDNA clone was obtained. Analysis of additional clones in the MM6 cDNA library revealed a second sequence that was identical to the 2.1 kb cDNA sequence first obtained from the 5' UTR through the purative seventh transmembrane domain but contained a different cytoplasmic tail. The second sequence appears to represent alternative splicing of the carboxyl-terminal tail of the MCP-1RA protein.	XX	
CC	XX	The two sequences are denoted MCP-1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol. wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN	XX	
CC	XX	WPI; 2001-626256/72.	XX	
CC	XX	Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.	XX	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 14:21:06 ; Search time 25 Seconds

(without alignments)

455.411 Million cell updates/sec

Title: US-10-791-592-2

Perfect score: 374

Sequence: 1 MLSTRSRFRINTNESGEEV.....GKGSIGRAPPASLDQKEA 374

Scoring Table: Oligo 10

Gapop 60.0 , Gapext 60.0

Searched: 180008 seqs, 30441898 residues

Word size: 10

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 90 summaries

Database : Published Applications AA_New:
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 8: /S1D55/ picodata/2/_pubpa/_US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	374 100.0	374	7	US-11-127-877-60	Sequence 60, Appl1
2	39 10.4	352	7	US-11-068-686-20	Sequence 20, Appl1
3	26 7.0	352	6	US-10-995-561-523	Sequence 523, Appl1
4	26 7.0	352	7	US-11-068-686-20	Sequence 523, Appl1
5	23 6.1	352	7	US-11-127-877-61	Sequence 61, Appl1
6	23 6.1	216	6	US-10-995-561-522	Sequence 522, Appl1
7	22 5.9	355	7	US-11-127-877-64	Sequence 64, Appl1
8	22 5.9	355	7	US-11-127-877-64	Sequence 64, Appl1
9	22 5.9	355	7	US-11-216-610-2	Sequence 2, Appl1
10	22 5.9	355	7	US-11-216-610-4	Sequence 4, Appl1
11	22 5.9	355	7	US-11-216-610-6	Sequence 6, Appl1
12	12 3.2	360	6	US-10-959-710-36	Sequence 36, Appl1
13	12 3.2	360	7	US-11-144-731-1	Sequence 1, Appl1
14	12 3.2	360	7	US-11-262-284-34	Sequence 34, Appl1
15	10 2.7	346	7	US-11-157-930-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
 Sequence 60, Application US/11127877
 Publication No. US20050287565A1
 GENERAL INFORMATION:
 CORRESPONDENCE ADDRESS:
 ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 630 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/068, 686
 FILING DATE: 28-Feb-2005
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/33670
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELFAX: 312-474-6300
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 MOLECULE DESCRIPTION: SEQ ID NO: 20:
 US-11-068-686-20

Query Match 10.4%; Score 39; DB 7; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.1e-31; Length 352;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 GIFFTILITDRLTIAVHAFALKARTVFGVVTIVW 165

Db 115 GIFFTILITDRLTIAVHAFALKARTVFGVVTIVW 153

RESULT 3
 US-10-991-561-523

Sequence 523, Application US/10995561

Publication No. US2005027054A1

GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: C101559

CURRENT APPLICATION NUMBER: US/10/995,561

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 523

LENGTH: 352

TYPE: PRT

ORGANISM: Homo sapiens

US-10-991-561-523

Query Match 7.0%; Score 26; DB 6; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11; Length 352;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 MVICYSGIILKLTLLRNEKCRHRAVR 243

Db 210 MVICYSGIILKLTLLRNEKCRHRAVR 235

RESULT 4
 US-11-068-686-2

Sequence 2, Application US/11086866

Publication No. US20050260565A1

GENERAL INFORMATION:
 APPLICANT: Gray, Patrick W.
 Schweickart, Vicky L.
 Report, Carol J.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/068, 686
 FILING DATE: 28-Feb-2005
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/33670
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELFAX: 312-474-6300
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 MOLECULE DESCRIPTION: SEQ ID NO: 2:
 US-11-068-686-2:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 MOLECULE DESCRIPTION: SEQ ID NO: 2:
 US-11-068-686-2:
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: /="8BC amino acid sequence"
 OTHER INFORMATION: SEQ ID NO: 2:
 US-11-068-686-2:
 Query Match 7.0%; Score 26; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 218 MVICYSGIILKLTLLRNEKCRHRAVR 243
 Db 210 MVICYSGIILKLTLLRNEKCRHRAVR 235
 RESULT 5
 US-11-127-877-61
 Sequence 61, Application US/11127877
 Publication No. US20050287565A1
 GENERAL INFORMATION:
 APPLICANT: Marchiers, Pascal G.
 APPLICANT: Hoffmann, Marcel
 APPLICANT: Spitaels, Koenraad F. P.
 APPLICANT: Laenen, Wendy
 TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
 Best Local Similarity 100.0%; Pred. No. 2.9e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 218 MVICYSGIILKLTLLRNEKCRHRAVR 243
 Db 210 MVICYSGIILKLTLLRNEKCRHRAVR 235
 NUMBER OF SEQ ID NOS: 590
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 61
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-127-877-61
 Query Match 7.0%; Score 26; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 218 MVICYSGIILKLTLLRNEKCRHRAVR 243

Result No.	Score	Query	Match	Length	DB	ID	Description
1	374	100.0	374	3	US-09-893-512-13		Sequence 13, App1
:	2	374	100.0	374	4	US-10-039-659-14	Sequence 14, App1
;	3	374	100.0	374	4	US-10-239-423-63	Sequence 63, App1
	4	374	100.0	374	4	US-10-754-071-14	Sequence 14, App1
	5	374	100.0	374	4	US-10-741-601-287	Sequence 287, App1
	6	374	100.0	374	5	US-10-791-592-2	Sequence 2, App1
	7	374	100.0	374	5	US-10-791-166-2	Sequence 2, App1
	8	374	100.0	374	5	US-10-759-860-14	Sequence 14, App1
	9	374	100.0	374	5	US-10-799-736-13	Sequence 13, App1
	10	374	100.0	374	5	US-10-988-267-2	Sequence 2, App1
	11	374	100.0	374	5	US-10-773-446-126	Sequence 126, App1
	12	374	100.0	374	5	US-10-287-436A-387	Sequence 387, App1
	13	374	100.0	374	5	US-10-287-436A-1087	Sequence 1087, App1
	14	374	100.0	374	6	US-11-021-951-161	Sequence 161, App1
	15	344	92.0	344	3	US-09-779-879A-9	Sequence 9, App1
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	17	344	92.0	344	4	US-10-232-686-9	Sequence 9, App1
	18	344	92.0	344	4	US-10-067-800-9	Sequence 9, App1
	19	344	92.0	344	4	US-10-135-839-9	Sequence 9, App1
	20	344	92.0	344	5	US-10-994-679-9	Sequence 9, App1
	21	344	92.0	359	5	US-10-988-267-24	Sequence 24, App1
	22	313	83.7	360	3	US-09-131-827A-2	Sequence 2, App1
	23	313	83.7	360	4	US-10-225-567A-460	Sequence 460, App1
	24	313	83.7	360	4	US-10-164-649-50	Sequence 50, App1
	25	313	83.7	360	4	US-10-239-423-64	Sequence 64, App1
	26	313	83.7	360	4	US-10-439-845-8	Sequence 8, App1
	27	313	83.7	360	4	US-10-741-601-285	Sequence 285, App1

ALIGNMENTS

RESULT 1
 US-09-893-512-13
 ; Sequence 13, Application US/09893512
 ; Publication No. US20030017530A1
 ; GENERAL INFORMATION:

APPLICANT: OWMAN, CHRISTIE
 TITLE OF INVENTION: REPTHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
 FILE REFERENCE: 7/55.0001-03 SEQUENCE LISTING
 CURRENT FILING DATE: 2001-06-29
 PTOF APPLICATION NUMBER: 60/061,789
 PTOF FILING DATE: 1997-10-14
 PTOF APPLICATION NUMBER: 60/081,958
 PTOF FILING DATE: 1998-04-15
 PTOF APPLICATION NUMBER: 09/170,069
 PTOF FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 13
 LENGTH: 374
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-893-512-13

Query Match 100.0%: Score 374; DB 3; Length 374;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 374; Conservative 0; Gaps 0;
 Mismatches 374; Indels 0; Gaps 0;

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 Db 1 MLSPRSRSRPRNTNESGEVTTFDDYDCAPICKPDKVQIGAQOLLPLPLSIVLPIRGWGN 60
 Qy 61 MLVVLINCKLKLTDYLNLIAISDILFLITLPLWHSAAANEVGNAMCKLFLGKLY 120
 Db 61 MLVVLINCKLKLTDYLNLIAISDILFLITLPLWHSAAANEVGNAMCKLFLGKLY 120
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 Db 121 HIGYFGGIFFLITLIDRYLIAVFAVFKARTVTFGTVTSVTLWVAFASVPGIIFTK 180
 Qy 181 COKEDSVYTCGPYFPRGNNNFTIMRNILGVLPLIMIVCYSGILKTKLRCNEKEKRR 240
 Db 181 COKEDSVYTCGPYFPRGNNNFTIMRNILGVLPLIMIVCYSGILKTKLRCNEKEKRR 240
 Qy 241 AVRIFTIMIVYFLETPNIVILANTDFFGLNSNCBTSQDQATOVTETLGTMTHCC 300
 Db 241 AVRIFTIMIVYFLETPNIVILANTDFFGLNSNCBTSQDQATOVTETLGTMTHCC 300
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRIAPILOPKVPGPVGTVREPKVNGKTVTQGLDGRGKGSI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIAPILOPKVPGPVGTVREPKVNGKTVTQGLDGRGKGSI 360
 Qy 361 GRAPEASLDQKEGA 374
 Db 361 GRAPEASLDQKEGA 374

RESULT 2
 US-10-039-659-14
 Sequence 14, Application US/10039659
 Publication No. US20030167A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Wei
 Gish, Kurt C.
 Schall, Thomas J.
 Vicari, Alain P.
 Zornik, Albert

NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/039,659
 FILING DATE: 03-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/887,977
 FILING DATE: 03-JUL-1997
 APPLICATION NUMBER: US 60/021,644
 FILING DATE: 05-JUL-1996
 APPLICATION NUMBER: US 60/028,329
 FILING DATE: 11-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0589K1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-852-9192
 TELEFAX: 650-496-1200
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-10-039-659-14

Query Match 100.0%: Score 374; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 374; Conservative 0; Gaps 0;
 Mismatches 374; Indels 0; Gaps 0;

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 Db 1 MLSTRSRSRPRNTNESGEVTTFDDYDCAPICKPDKVQIGAQOLLPLPLSIVLPIRGWGN 60
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 Db 61 HIGYFGGIFFLITLIDRYLIAVFAVFKARTVTFGTVTSVTLWVAFASVPGIIFTK 180
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 Db 181 AVRIFTIMIVYFLETPNIVILANTDFFGLNSNCBTSQDQATOVTETLGTMTHCC 300
 Qy 241 NPIIYAFVGEKFRSLFHIALGCRIAPILOPKVPGPVGTVREPKVNGKTVTQGLDGRGKGSI 360
 Db 241 NPIIYAFVGEKFRSLFHIALGCRIAPILOPKVPGPVGTVREPKVNGKTVTQGLDGRGKGSI 360
 Qy 301 GRAPEASLDQKEGA 374
 Db 301 GRAPEASLDQKEGA 374

RESULT 3
 US-10-39-423-63
 Sequence 63, Application US/10239423
 Publication No. US20030166894A
 GENERAL INFORMATION:
 APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMAN, Knut;
 APPLICANT: HELLMAND, Aleksandra; SPODSBERG, Nikolaj
 TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the

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GenCore version 5.1.7

OM protein - protein search, using sw mode1

Run on: March 29, 2006, 14:08:45 ; Search time 46 Seconds

(without alignments)
672.189 Million cell updates/sec

Scoringtable: **GNCGC** Gapop 60.0 , Gapext 60.0

Perfect score: 374

Sequence: 1 MLLTSRSRFIRNTNESGEEV GKGRKSTGRAPAEASLQDKEGA 374

Word size: 8

Sto

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 90 summaries

Database : Issued_Patents_AA:*

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6: /cgn2_6/podata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
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2	374	100.0	374	2	US-08-446-669-2		Sequence 2, Appli
3	374	100.0	374	2	US-10-039-659A-14		Sequence 14, Appli
4	374	100.0	374	2	US-09-625-573-2		Sequence 2, Appli
5	374	100.0	374	4	PCT-US95-00476-2		Sequence 2, Appli
6	374	100.0	387	2	US-09-949-016-11222		Sequence 11222, A
7	344	92.0	344	2	US-08-466-343D-9		Sequence 9, Appli
8	344	92.0	344	2	US-09-502-784A-9		Sequence 9, Appli
9	83.7	83.7	360	1	US-08-393A-4		Sequence 4, Appli
10	313	83.7	360	2	US-08-446-669-4		Sequence 4, Appli
11	313	83.7	360	2	US-09-045-583-50		Sequence 50, Appli
12	83.7	83.7	360	2	US-09-534-185-50		Sequence 50, Appli
13	313	83.7	360	2	US-09-131-827A-20		Sequence 20, Appli
14	313	83.7	360	2	US-09-502-783A-9		Sequence 2, Appli
15	83.7	83.7	360	4	PCT-US95-00476-4		Sequence 4, Appli
16	313	83.7	377	2	US-09-949-016-11221		Sequence 11221, A
17	300	80.2	347	1	US-08-461-244-3		Sequence 3, Appli
18	249	66.6	360	2	US-09-826-509-473		Sequence 473, Appli
19	241	64.4	360	2	US-09-826-509-473		Sequence 473, Appli
20	224	59.9	329	2	US-09-502-783A-9		Sequence 9, Appli
21	224	59.9	329	2	US-09-339-912A-9		Sequence 4, Appli
22	224	59.9	329	2	US-09-625-573-4		Sequence 4, Appli
23	194	51.9	360	2	US-08-933-752-7		Sequence 7, Appli
24	194	51.9	360	2	US-09-938-719-7		Sequence 7, Appli
25	194	51.9	360	2	US-09-938-226B-7		Sequence 7, Appli
26	194	51.9	360	2	US-09-703B-7		Sequence 13, Appli
27	83	22.2					Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-450-393A-2
Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:

APPLICANT: Charo, Israel
 APPLICANT: Coughlin, Shaun
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,393A
 FILING DATE: May 25, 1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Clegg, Luann
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: UCAL-237/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5165
 TELEFAX: 415-857-0663
 TELEX: 380816cooleypa
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-450-393A-2

Query Match 100.0% Score 374; DB 1; Length 374;

Best Local Similarity 100.0% Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 374; Conservative 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MLSTSRSRPIRTNTESGEVTTFFDYDGAQCKFDVKIGAQQLPPLYSVLPFIRGVGN 60
 Db 1 MLSTSRSRPIRTNTESGEVTTFFDYDGAQCKFDVKIGAQQLPPLYSVLPFIRGVGN 60
 Qy 1 MLVVLILINCKLKCLTDYLLNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKLKCLTDYLLNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLY 120
 Qy 121 HIGYGGIPPIFLITIDRLAIIAVPAKARTYFGVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGYGGIPPIFLITIDRLAIIAVPAKARTYFGVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVTVCGPYPRGMNNFTIMRNFLPQFPLGNSCESTQDQATVTEFLGMTHCC1 300
 Db 241 AYRVLFTIMIVPLFWPPNIVLNPQFPLGNSCESTQDQATVTEFLGMTHCC1 300
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 Db 241 AYRVLFTIMIVPLFWPPNIVLNPQFPLGNSCESTQDQATVTEFLGMTHCC1 300
 Qy 301 NPIIYAFGEKFRSLFHALGCRAPLQKPVCGPFGURGKAVKTIQGLDGRGKGS1 360
 Db 301 NPIIYAFGEKFRSLFHALGCRAPLQKPVCGPFGURGKAVKTIQGLDGRGKGS1 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

Query Match 100.0% Score 374; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MLSTSRSRPIRTNTESGEVTTFFDYDGAQCKFDVKIGAQQLPPLYSVLPFIRGVGN 60
 Db 1 MLSTSRSRPIRTNTESGEVTTFFDYDGAQCKFDVKIGAQQLPPLYSVLPFIRGVGN 60
 Qy 61 MLVVLILINCKLKCLTDYLLNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKLKCLTDYLLNLAISDLFLITPLWAHSAAANEWFGNAMCKLFTGLY 120
 Qy 121 HIGYGGIPPIFLITIDRLAIIAVPAKARTYFGVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGYGGIPPIFLITIDRLAIIAVPAKARTYFGVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVTVCGPYPRGMNNFTIMRNFLPQFPLGNSCESTQDQATVTEFLGMTHCC1 300
 Db 241 AYRVLFTIMIVPLFWPPNIVLNPQFPLGNSCESTQDQATVTEFLGMTHCC1 300
 Qy 301 NPIIYAFGEKFRSLFHALGCRAPLQKPVCGPFGURGKAVKTIQGLDGRGKGS1 360
 Db 301 NPIIYAFGEKFRSLFHALGCRAPLQKPVCGPFGURGKAVKTIQGLDGRGKGS1 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 2
 US-08-446-669-2
 ; Sequence 2, Application US/08446669